

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Biocelebration Ltd.

OM protein - protein search, using SW model

Run on: May 5, 2006, 00:24:47 ; Search time 47 Seconds  
(without alignments)  
687.791 Million cell updates/sec

Title: US-10-057-532A-7  
Perfect score: 2071  
Sequence: 1 MAHHHHHPPGSGSGGTMAIS.....TCECTKPDSPYLPFDGIFCSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
1: /cgn2\_6/ptodata/1/1aa/5-COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/6-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PTCUTS-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RE-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfilltest.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2071	100.0	391	2	US-10-057-531A-7 Sequence 7, Appli
2	2055	99.2	393	2	US-10-057-531A-3 Sequence 3, Appli
3	2008.5	97.0	431	2	US-10-057-531A-2 Sequence 2, Appli
4	2008.5	97.0	546	2	US-10-057-531A-1 Sequence 1, Appli
5	1970	95.1	375	2	US-09-710-000-8 Sequence 8, Appli
6	1968	95.0	383	2	US-10-057-531A-5 Sequence 5, Appli
7	1931	93.2	394	2	US-08-195-705-2 Sequence 2, Appli
8	1931	93.2	394	2	US-09-500-376-2 Sequence 2, Appli
9	1928	93.1	402	2	US-09-500-376-16 Sequence 16, Appli
10	1921	92.8	394	2	US-08-195-705-4 Sequence 4, Appli
11	1921	92.8	394	2	US-09-500-376-3 Sequence 3, Appli
12	1166.5	56.3	613	2	US-09-117-415B-22 Sequence 22, Appli
13	1166.5	56.3	631	2	US-09-117-415B-18 Sequence 18, Appli
14	1166.5	56.3	631	2	US-09-117-415B-20 Sequence 20, Appli
15	1166.5	56.3	649	2	US-09-117-415B-16 Sequence 16, Appli
16	1166.5	56.3	1602	2	US-09-269-874A-7 Sequence 7, Appli
17	1166.5	56.3	1621	2	US-09-269-874A-5 Sequence 5, Appli
18	1166.5	56.3	1639	2	US-09-269-874A-3 Sequence 3, Appli
19	1163.5	56.2	384	2	US-09-500-376-8 Sequence 8, Appli
20	1161.5	56.1	355	2	US-09-175-684A-9 Sequence 9, Appli
21	1161.5	56.0	361	2	US-09-175-684A-10 Sequence 10, Appli
22	1159.5	55.6	594	2	US-09-117-415B-2 Sequence 2, Appli
23	1154.5	55.7	379	2	US-09-175-684A-11 Sequence 11, Appli
24	1040	50.2	377	2	US-08-195-705-5 Sequence 5, Appli
25	1040	50.2	377	2	US-09-500-376-5 Sequence 5, Appli
26	986	47.6	375	2	US-08-195-705-3 Sequence 3, Appli
27	986	47.6	375	2	US-09-500-376-4 Sequence 4, Appli

28	788	38.0	380	2	US-09-125-031C-12 Sequence 12, Appli
29	777	37.5	380	2	US-09-125-031C-13 Sequence 13, Appli
30	734.5	35.5	379	2	US-09-125-031C-11 Sequence 11, Appli
31	527	25.4	108	2	US-09-125-031C-10 Sequence 10, Appli
32	527	25.4	116	2	US-09-125-031C-5 Sequence 5, Appli
33	523	25.3	95	2	US-09-125-031C-2 Sequence 2, Appli
34	523	25.3	127	2	US-09-125-031C-8 Sequence 8, Appli
35	424.5	20.5	281	2	US-09-125-031C-14 Sequence 14, Appli
36	288	13.9	53	1	US-08-290-919-4 Sequence 4, Appli
37	277	13.4	48	1	US-08-290-919-12 Sequence 12, Appli
38	274	13.2	48	1	US-08-290-919-2 Sequence 2, Appli
39	272	13.1	53	1	US-08-290-919-3 Sequence 3, Appli
40	271	13.1	48	1	US-08-290-919-1 Sequence 1, Appli
41	256.5	12.4	106	1	US-08-290-919-11 Sequence 11, Appli
42	187.5	9.1	350	2	US-09-763-397A-2 Sequence 2, Appli
43	145	7.0	630	2	US-09-248-796A-20275 Sequence 20275, A
44	139.5	6.7	496	2	US-09-543-681A-6465 Sequence 6465, Ap
45	139.5	6.7	1010	2	US-09-134-001C-5178 Sequence 5178, Ap

## ALIGNMENTS

RESULT 1  
US-10-057-531A-7  
; Sequence 7, Application US/10057531A  
; Patent No. 6855322  
; GENERAL INFORMATION:  
; APPLICANT: Lyon, Jeffrey A.  
; TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite  
; TITLE OF INVENTION: Protein-142 Vaccine  
; FILE REFERENCE: 003/241/SAP  
; CURRENT APPLICATION NUMBER: US/10/057,531A  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/264,535  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/347,564  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 7  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: E. coli expressed P. falciparum MSP-142 (3D7)  
US-10-057-531A-7

Query Match 100.0%; Score 2071; DB 2; Length 391;  
Best local similarity 100.0%; Pred. No. 5,8e-149; Mismatches 0; Indels 0; Gaps 0;  
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAHHHHHPPGSGSGGTMAISVTMDNIISGFENEYDVILKPLAGVRSKKQIEKNITF	60
DB	1	MAHHHHHPPGSGSGGTMAISVTMDNIISGFENEYDVILKPLAGVRSKKQIEKNITF	60
QY	61	NLNINDIINSLLKRRKTYLDVLESDFMOFKIISSENYIIEISFGLNSEQNTLLKSYKY	120
DB	61	NLNINDIINSLLKRRKTYLDVLESDFMOFKIISSENYIIEISFGLNSEQNTLLKSYKY	120
QY	121	IKESVENDIKPAQGISYKEVKLAKYKDDLESIKKVIKEEKEKPPSPPTPPSPAKTDE	180
DB	121	IKESVENDIKPAQGISYKEVKLAKYKDDLESIKKVIKEEKEKPPSPPTPPSPAKTDE	180
QY	181	QKESKFLPFLTNIETLYNNLVNKIDYLLNLKAKINDCNVEKDAHVKTYSDLKAID	240
DB	181	QKESKFLPFLTNIETLYNNLVNKIDYLLNLKAKINDCNVEKDAHVKTYSDLKAID	240
QY	241	DKIDLPKVPFEAKIKULINDTKKDMGLKLTSGLVQNPNTTIIISKLIBGKPDMLNIS	300
DB	241	DKIDLPKVPFEAKIKULINDTKKDMGLKLTSGLVQNPNTTIIISKLIBGKPDMLNIS	300

QY 301 OHQCVKQCPENSGCFRHLDEREBCCLNLYKQBGDKVENPPTCNENNGCCDADATCT 360  
DB 301 OHQCVKQCPENSGCFRHLDEREBCCLNLYKQBGDKVENPPTCNENNGCCDADATCT 360  
QY 361 BEDSGSSRRKKTCTECTKPDSPYPLFDGIFCSS 391  
DB 361 BEDSGSSRRKKTCTECTKPDSPYPLFDGIFCSS 391

## RESULT 2

US-10-057-531A-3  
; Sequence 3, Application US/10057531A  
; Patent No. 6855322  
; GENERAL INFORMATION:  
; APPLICANT: Lyon, Jeffrey A.  
; APPLICANT: Angov, Evelina  
; TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite  
; FILE REFERENCE: 003/241/SAP  
; CURRENT APPLICATION NUMBER: US/10/057,531A  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/264,535  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/347,564  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 3  
; LENGTH: 393  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein  
; OTHER INFORMATION: Sequence in pET42A  
; Patent No. 6855322  
US-10-057-531A-3

Query Match 99.2%; Score 2055; DB 2; Length 393;  
Best Local Similarity 99.2%; Pred. No. 9,6e-148;  
Matches 390; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 MAHHHHHPGGS--GSGTMAISVTMDNIIISGFENEVDIYLLKPLAGVYRSLLKKQIEKNIF 58  
DB 1 MAHHHHHPGGSIEGRGTMAISVTMDNIIISGFENEVDIYLLKPLAGVYRSLLKKQIEKNIF 60  
QY 59 TENLNLDIILNSRLKKRYKFLDVESDLMQFKHISNEIIEDSKLINSBOKNTLLKSY 118  
DB 61 TENLNLDIILNSRLKKRYKFLDVESDLMQFKHISNEIIEDSKLINSBOKNTLLKSY 120  
QY 119 KYIKESVENDIKFAQEGISYEKVLAKYKDLESIKVYKEKEKFPSSPTTPSPAKT 178  
DB 121 KYIKESVENDIKFAQEGISYEKVLAKYKDLESIKVYKEKEKFPSSPTTPSPAKT 180  
QY 179 DBQKESKFLPLTLNIEFLYNNLVNKIDYILNLAKINDCNVEKDEAHVKTITKLSDLKA 238  
DB 181 DBQKESKFLPLTLNIEFLYNNLVNKIDYILNLAKINDCNVEKDEAHVKTITKLSDLKA 240  
QY 239 IDDKTDLFKNPYDFEAIKKLINDPTKMDLGLKLTSGLVONFPNTIISKLEGRFQDMLN 298  
DB 241 IDDKTDLFKNPYDFEAIKKLINDPTKMDLGLKLTSGLVONFPNTIISKLEGRFQDMLN 300  
QY 299 ISOHCYKQCPENSGCFRHLDEREBCCLNLYKQBGDKVENPPTCNENNGCCDADAT 358  
DB 301 ISOHCYKQCPENSGCFRHLDEREBCCLNLYKQBGDKVENPPTCNENNGCCDADAT 360  
QY 359 CTEEDSGSSRRKKTCTECTKPDSPYPLFDGIFCSS 391  
DB 361 CTEEDSGSSRRKKTCTECTKPDSPYPLFDGIFCSS 393

RESULT 3  
US-10-057-531A-2  
; Sequence 2, Application US/10057531A

; Patent No. 6855322  
; GENERAL INFORMATION:  
; APPLICANT: Lyon, Jeffrey A.  
; APPLICANT: Angov, Evelina  
; TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite  
; FILE REFERENCE: 003/241/SAP  
; CURRENT APPLICATION NUMBER: US/10/057,531A  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/264,535  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/347,564  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 2  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein  
; OTHER INFORMATION: Sequence in pET150/MSP1-42  
; Patent No. 6855322  
US-10-057-531A-2

Query Match 97.0%; Score 2008.5; DB 2; Length 431;  
Best Local Similarity 89.5%; Pred. No. 3,6e-144;  
Matches 385; Conservative 0; Mismatches 4; Indels 41; Gaps 1;

QY 3 HHHHHHPGGS-----GSGTMAISV 21  
DB 2 HHHHHHPGGSGLVPRSGMKETAARERQMDSPDGTDDDKAMADIGSIEGRGTMAISV 61  
QY 22 TMDNIIISGFENEVDIYLLKPLAGVYRSLLKKQIEKNIFTENLNLDIILNSRLKKRYFLDV 81  
DB 62 TMDNIIISGFENEVDIYLLKPLAGVYRSLLKKQIEKNIFTENLNLDIILNSRLKKRYFLDV 121  
QY 82 LESDLMQFKHISNEIIEDSKLINSBOKNTLLKSYKYIKESVENDIKFAQEGISYEK 141  
DB 122 LESDLMQFKHISNEIIEDSKLINSBOKNTLLKSYKYIKESVENDIKFAQEGISYEK 181  
QY 142 VLAKYKDDLESIKVYKEKEKFPSSPTTPSPAKTDBQKESKFLPLTLNIEFLYNNL 201  
DB 182 VLAKYKDDLESIKVYKEKEKFPSSPTTPSPAKTDBQKESKFLPLTLNIEFLYNNL 241  
QY 202 VNKTIDYILNLAKINDCNVEKDEAHVKTITKLSDLKAIIDKIDLPKNPYDFEAIKKLIND 261  
DB 242 VNKTIDYILNLAKINDCNVEKDEAHVKTITKLSDLKAIIDKIDLPKNPYDFEAIKKLIND 301  
QY 262 DTKDMLGLKLTSGLVONFPNTIISKLEGRFQDMLNISOHCYKQCPENSGCFRHLDE 321  
DB 302 DTKDMLGLKLTSGLVONFPNTIISKLEGRFQDMLNISOHCYKQCPENSGCFRHLDE 361  
QY 322 REECKCLNLYKQBGDKVENPPTCNENNGCCDADATCTEEDSGSSRRKKTCTECTKPDSPY 381  
DB 362 REECKCLNLYKQBGDKVENPPTCNENNGCCDADATCTEEDSGSSRRKKTCTECTKPDSPY 421  
QY 382 PLFDGIFCSS 391  
DB 422 PLFDGIFCSS 431

RESULT 4  
US-10-057-531A-1  
; Sequence 1, Application US/10057531A  
; Patent No. 6855322  
; GENERAL INFORMATION:  
; APPLICANT: Lyon, Jeffrey A.  
; APPLICANT: Angov, Evelina  
; TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite  
; FILE REFERENCE: 003/241/SAP  
; CURRENT APPLICATION NUMBER: US/10/057,531A

```
.; CURRENT FILING DATE: 2002-01-25
.; PRIOR APPLICATION NUMBER: US 60/264,535
.; PRIOR FILING DATE: 2001-01-26
.; PRIOR APPLICATION NUMBER: US 60/347,564
.; PRIOR FILING DATE: 2001-10-26
.; NUMBER OF SEQ ID NOS: 12
.; SOFTWARE: Apple Macintosh Microsoft Word 6.0
.; SEQ ID NO 1
.; LENGTH: 546
.; TYPE: PRT
.; ORGANISM: Artificial sequence
.; FEATURE:
.; OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein
.; Patent No. 6855322
US-10-057-531A-1
```

```
Query Match          97.0%; Score 2008.5; DB 2; Length 546;
Best Local Similarity 89.5%; Pred. No. 4,9e-144;
Matches 385; Conservative 0; Mismatches 4; Indels 41; Gaps 1;
```

```
QY 3 HHHHHHPCG-----SSGCTMAISV 21
Db 117 HHHHHSSGLVPRGSGMKETAARERQHMDSPDIGTDDDKAMADISIEGRGTMAISV 176
QY 22 TMDNIIISGFENEVDVYILKPLAGVYRSLLKQIEKNIFFTNLNLNDILNSRLKKRYFLDV 81
Db 177 TMDNIIISGFENEVDVYILKPLAGVYRSLLKQIEKNIFFTNLNLNDILNSRLKKRYFLDV 236
QY 82 LESDLMQFKHISSENYIIEDSFKLNSQKNTLLSKYIKESVENDIKFAQEGISYEEK 141
Db 237 LESDLMQFKHISSENYIIEDSFKLNSQKNTLLSKYIKESVENDIKFAQEGISYEEK 296
QY 142 VLAKYKDDLSEIKKYIKEREKRPSSPTTPSPAKTDEQKESKFLPLTNIEFLYNNL 201
Db 297 VLAKYKDDLSEIKKYIKEREKRPSSPTTPSPAKTDEQKESKFLPLTNIEFLYNNL 356
QY 202 VNKIDIDYILNIAKAKINDCNVEKDEAHVKITKLSDLKAIIDDKIDLFKNPYDFEAIKGLND 261
Db 357 VNKIDIDYILNIAKAKINDCNVEKDEAHVKITKLSDLKAIIDDKIDLFKNPYDFEAIKGLND 416
QY 262 DTKXDMIGKLLSTGLVQNFPTTIISKLIEGKFQDMNLISQHCVCVKQCPENSGCFRHLDE 321
Db 417 DTKXDMIGKLLSTGLVQNFPTTIISKLIEGKFQDMNLISQHCVCVKQCPENSGCFRHLDE 476
QY 322 REECKCLINYOEGDKCVENPPTNENNGGCDADATCTEEDSGSSRKKITCECTKPDYSY 381
Db 477 REECKCLINYOEGDKCVENPPTNENNGGCDADATCTEEDSGSSRKKITCECTKPDYSY 536
QY 382 PLFDGIFCSS 391
Db 537 PLFDGIFCSS 546
```

RESULT 5

US-09-710-000-8

Sequence 8, Application US/09710000

Patent No. 6660498

GENERAL INFORMATION:

APPLICANT: Hui, George, S.N.

APPLICANT: Ho, Walter K.K.

APPLICANT: Lab-Yin, Pang

TITLE OF INVENTION: Malaria Vaccine

FILE REFERENCE: 23461-2001100

CURRENT APPLICATION NUMBER: US/09/710,000

CURRENT FILING DATE: 2000-11-10

PRIOR APPLICATION NUMBER: 60/226,861

PRIOR FILING DATE: 2000-08-22

PRIOR APPLICATION NUMBER: 60/165,178

PRIOR FILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/168,327

PRIOR FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 11

```
.; SOFTWARE: FastSeq for Windows Version 4.0
.; SEQ ID NO 8
.; LENGTH: 375
.; TYPE: PRT
.; ORGANISM: Unknown
.; FEATURE:
.; OTHER INFORMATION: amino acid sequence of PfMSP-142
US-09-710-000-8
```

```
Query Match          95.1%; Score 1970; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.5e-141;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 17 MAISTVMNIIISGFENEVDVYILKPLAGVYRSLLKQIEKNIFFTNLNLNDILNSRLKKRK 76
Db 1 MAISTVMNIIISGFENEVDVYILKPLAGVYRSLLKQIEKNIFFTNLNLNDILNSRLKKRK 60
QY 77 YFLDVLESDDLQFKHISSENYIIEDSFKLNSQKNTLLSKYIKESVENDIKFAQEGI 136
Db 61 YFLDVLESDDLQFKHISSENYIIEDSFKLNSQKNTLLSKYIKESVENDIKFAQEGI 120
QY 137 SYEKVILAKYKDDLSEIKKYIKEREKRPSSPTTPSPAKTDEQKESKFLPLTNIEFL 196
Db 121 SYEKVILAKYKDDLSEIKKYIKEREKRPSSPTTPSPAKTDEQKESKFLPLTNIEFL 180
QY 197 LNNLVLNKKIDYILNIAKAKINDCNVEKDEAHVKITKLSDLKAIIDDKIDLFKNPYDFEAIK 256
Db 181 LNNLVLNKKIDYILNIAKAKINDCNVEKDEAHVKITKLSDLKAIIDDKIDLFKNPYDFEAIK 240
QY 257 KLINDITKXDMIGKLLSTGLVQNFPTTIISKLIEGKFQDMNLISQHCVCVKQCPENSGCF 316
Db 241 KLINDITKXDMIGKLLSTGLVQNFPTTIISKLIEGKFQDMNLISQHCVCVKQCPENSGCF 300
QY 317 RHLDERECKCLINYOEGDKCVENPPTNENNGGCDADATCTEEDSGSSRKKITCECT 376
Db 301 RHLDERECKCLINYOEGDKCVENPPTNENNGGCDADATCTEEDSGSSRKKITCECT 360
QY 377 KPDSYPLFDGIFCSS 391
Db 361 KPDSYPLFDGIFCSS 375
```

RESULT 6

US-10-057-531A-5

Sequence 5, Application US/10057531A

Patent No. 6855322

GENERAL INFORMATION:

APPLICANT: Lyon, Jeffrey A.

APPLICANT: Angov, Evelina

TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite

FILE REFERENCE: 003/241/SAP

CURRENT APPLICATION NUMBER: US/10/057,531A

CURRENT FILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: US 60/264,535

PRIOR FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: US 60/347,564

PRIOR FILING DATE: 2001-10-26

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Apple Macintosh Microsoft Word 6.0

SEQ ID NO 5

LENGTH: 383

TYPE: PRT

ORGANISM: Plasmodium falciparum 3D7 MSP142

US-10-057-531A-5

```
Query Match          95.0%; Score 1968; DB 2; Length 383;
Best Local Similarity 99.2%; Pred. No. 3.6e-141;
Matches 376; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 13 GSGTMAISVTMDNIIISGFENEVDVYILKPLAGVYRSLLKQIEKNIFFTNLNLNDILNSRL 72
Db 5 GSGTMAISVTMDNIIISGFENEVDVYILKPLAGVYRSLLKQIEKNIFFTNLNLNDILNSRL 64
```

Qy	73	KKRKFVLVLESDLMOPKHISSENYIIIESPFLKNSKNTLLKSKYKIKESYENDIKFA	132
Db	65	KKRKFVLVLESDLMOPKHISSENYIIIESPFLKNSKNTLLKSKYKIKESYENDIKFA	124
Qy	133	QEGISYIEKVLAKYKODLESIKKVIKEEKEKFPSPPTTTPPSPAKTDEOKESKFLPFLT	192
Db	125	QEGISYIEKVLAKYKODLESIKKVIKEEKEKFPSPPTTTPPSPAKTDEOKESKFLPFLT	184
Qy	193	NIETLYNNLVNKIIDYILNLKAKINDCNYEKDEAHVKITKLSDLKAIDDKIDLFKNPYDF	252
Db	185	NIETLYNNLVNKIIDYILNLKAKINDCNYEKDEAHVKITKLSDLKAIDDKIDLFKNPTDF	244
Qy	253	EAIKKLINDOTTKDMLGKILSTGLVONFPNTIISKLEBGFQDMLNISQHCYKQCPEN	312
Db	245	EAIKKLINDOTTKDMLGKILSTGLVONFPNTIISKLEBGFQDMLNISQHCYKQCPEN	304
Qy	313	SGCFPHLDERECCCKLLNKKOEGDKCVENPNTCNENNGCDADANCTEEDSGSSRRKIT	372
Db	305	SGCFPHLDERECCCKLLNKKOEGDKCVENPNTCNENNGCDADANCTEEDSGSSRRKIT	364
Qy	373	CECTKPDGYPLFDGIFCCSS 391	
Db	365	CECTKPDGYPLFDGIFCCSS 383	

```

US-08-195-705-2
Sequence 2, Application US/08195705
Patent No. 6420523
GENERAL INFORMATION:
APPLICANT: Chang, Sandra
APPLICANT: Hui, George
APPLICANT: Barr, Philip
APPLICANT: Gibson, Helen
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM
TITLE OF INVENTION: FALCIPARUM VACCINE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Davis Hoxie Faithfull Hapgood
STREET: 45 Rockefeller Pl.
CITY: New York
STATE: N.Y.
COUNTRY: USA
ZIP: 10111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,705
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32140
REFERENCE/DOCKET NUMBER: 11880A3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-757-2200
TELEFAX: 212-586-1461
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum

```

	Query Match	93.2%	Score 1931;	DB 2;	Length 394;
	Best Local Similarity	98.7%;	Pred. No. 2,4e-138;		
	Matches 369;	Conservative 1;	Mismatches 4;	Indels 0;	Gaps 0;
QY	18 AISTMTNIIISGFENEYDVIYLLKPLAGYRBLTKQIENIETFPNLNINDIINSRLKKRY				77
Db	1 AISTMTNIIISGFENEYDVIYLLKPLAGYRBLTKQIENIETFPNLNINDIINSRLKKRY				60
QY	78 FLVDIESDLMQFKIISSENYIIEDSFKLINSEQNTLLSKYKIKESYENDIKFAQEGIS				137
Db	61 FLVDIESDLMQFKIISSENYIIEDSFKLINSEQNTLLSKYKIKESYENDIKFAQEGIS				120
QY	138 YEKVLAKEYKODLESIKKVIKEKEKCPSSPPTTPSPAKTDEOKESKFLPFLNIETL				197
Db	121 YEKVLAKEYKODLESIKKVIKEKEKCPSSPPTTPSPAKTDEOKESKFLPFLNIETL				180
QY	198 YNNLVNKIIDVLLNLKAKINDCNEKQEAHYIKRLSPLKIIDDKIDLFKNPVPFAIKK				257
Db	181 YNNLVNKIIDVLLNLKAKINDCNEKQEAHYIKRLSPLKIIDDKIDLFKNHPFAIKK				240
QY	258 LINDDTKMDLGLKLSLSTGLVONFENTIIISKVIEGKFQDMLNISQHCYKQCPENSGFR				317
Db	241 LINDDTKMDLGLKLSLSTGLVONFENTIIISKVIEGKFQDMLNISQHCYKQCPENSGFR				300
QY	318 HLDREBECKLLNKKQEGDKCVENPNPTCNENNGCCDADATCTEEDSGSSRKKIITCECTK				377
Db	301 HLDREBECKLLNKKQEGDKCVENPNPTCNENNGCCDADACTEEDSGSSNGKIIITCECTK				360
QY	378 PDSYPLFDGIFCCSS 391				
Db	361 PDSYPLFDGIFCCSS 374				

```

RESULT 8
US-09-500-376--2
; Sequence 2, Application US/09500376
; Patent No. 6855316
; GENERAL INFORMATION:
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Baculovirus Produced Plasmodium Falciparum Vaccine
; FILE REFERENCE: A-67984
; CURRENT APPLICATION NUMBER: US/09/500.376
; CURRENT FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 08/195,705
; PRIOR FILING DATE: 1994-02-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRN
; ORGANISM: Plasmodium falciparum
US-09-500-376-2

Query Match          93.2%; Score 1931; DB 2; Length 394;
Best Local Similarity 98.7%; Pred. No. 2,4e-138;
Matches 369; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 18 AISTMTNITLISGGENEYDVYIKRLAGVYRSLKKOIEKNTFTFLNLINDILNSRLKKRY 77
    |||||||
Db 1 AISTMTNITLISGGENEYDVYIKRLAGVYRSLKKOIEKNTFTFLNLINDILNSRLKKRY 60
    |||||||

Oy 78 FLVDLESIDLMOFKIISSENYIIEDSPKLLNSEQKNTLLKSYKIKESYENDIKFAQEGIS 137
    |||||||
Db 61 FLVDLESIDLMOFKIISSENYIIEDSPKLLNSEQKNTLLKSYKIKESYENDIKFAQEGIS 120
    |||||||

Oy 138 YEEKVLAKYKODLESIKKVIKEEKKEKPPSPPTTPSPAKTDEQKESKFLPLTNITTL 197
    |||||||
Db 121 YEEKVLAKYKODLESIKKVIKEEKKEKPPSPPTTPSPAKTDEQKESKFLPLTNITTL 180
    |||||||

Oy 198 YNNLVAKIDYVILNLKAKKINDCNVKEQBAHKITKLSDLKAIDDKIDLFKNPYDFEAIKK 257
    |||||||

```



Db 181 YNNLVNKIDYILNKKAKINDCNVEKDEAHVITKLSDLKALDIDKIDLFKNHNDPEALIKK 240  
Qy 258 LINDTKKDMGLKLGSTLVONFPNTIISKLEGFQDMNLSOHQCVKQCPENSGCFR 317  
Db 241 LINDTKKDMGLKLGSTLVONFPNTIISKLEGFQDMNLSOHQCVKQCPENSGCFR 300  
Qy 318 HLDREBECKCLNLYKQEGDKCVENPNPTCNENNGGCDADATCTBEDSGSSRKITCECTK 377  
Db 301 HLDREBECKCLNLYKQEGDKCVENPNPTCNENNGGCDADATCTBEDSGSSRKITCECTK 360  
Qy 378 PDSYPLFDGIFCSS 391  
Db 361 PDSYPLFDGIFCSS 374

RESULT 9  
US-09-500-376-16  
; Sequence 16, Application US/09500376  
; Patent No. 6855316  
; GENERAL INFORMATION:  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Baculovirus Produced Plasmodium Falciiparum Vaccine  
; FILE REFERENCE: A-67984  
; CURRENT APPLICATION NUMBER: US/09/500,376  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: US 08/195,705  
; PRIOR FILING DATE: 1994-02-14  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 16  
; LENGTH: 402  
; TYPE: PRT  
; ORGANISM: Plasmodium falciiparum  
US-09-500-376-16

Query Match 93.1%; Score 1928; DB 2; Length 402;  
Best Local Similarity 98.1%; Pred. No. 4, 1e-138;  
Matches 368; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 16 TMAISVTMDNLSGFENEYDVIYLLKPLAGVYRSLLKQIEKNIFTFNLNLDILNSRLKKR 75  
Db 20 TMAISVTMDNLSGFENEYDVIYLLKPLAGVYRSLLKQIEKNIFTFNLNLDILNSRLKKR 79  
Qy 76 KYFLDVLSEDLMOFGHISSENEYIIDSFKLNSBQKNTLLSKYKIKESVENDIKFAQEG 135  
Db 80 KYFLDVLSEDLMOFGHISSENEYIIDSFKLNSBQKNTLLSKYKIKESVENDIKFAQEG 139  
Qy 136 ISYEKVLAKYKDDLESIKKVIKEEKEKPPSSPPTTPPSPAKTDEOKKESKFLPFLTNIE 195  
Db 140 ISYEKVLAKYKDDLESIKKVIKEEKEKPPSSPPTTPPSPAKTDEOKKESKFLPFLTNIE 199  
Qy 196 TLVNNLVNKIDYILNKKAKINDCNVEKDEAHVITKLSDLKALDIDKIDLFKNPYDEAIAI 255  
Db 200 TLVNNLVNKIDYILNKKAKINDCNVEKDEAHVITKLSDLKALDIDKIDLFKNHNDFAIAI 259  
Qy 256 KKLINDTKKDMGLKLGSTLVONFPNTIISKLEGFQDMNLSOHQCVKQCPENSGCFR 315  
Db 260 KKLINDTKKDMGLKLGSTLVONFPNTIISKLEGFQDMNLSOHQCVKQCPENSGCFR 319  
Qy 316 FRLHDERBECKCLNLYKQEGDKCVENPNPTCNENNGGCDADATCTBEDSGSSRKITCEC 375  
Db 320 FRLHDERBECKCLNLYKQEGDKCVENPNPTCNENNGGCDADATCTBEDSGSSRKITCEC 379  
Qy 376 TKPDSYPLFDGIFCS 390  
Db 380 TKPDSYPLFDGIFCS 394

RESULT 10  
US-08-195-705-4  
; Sequence 4, Application US/08195705  
; Patent No. 6420523

GENERAL INFORMATION:  
APPLICANT: Chang, Sandra  
APPLICANT: Hui, George  
APPLICANT: Bart, Philip  
APPLICANT: Gibson, Helen  
TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM  
TITLE OF INVENTION: FALCIPARUM VACCINE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Davis Hoxie Faithfull Hapgood  
STREET: 45 Rockefeller Pl.  
CITY: New York  
STATE: N.Y.  
COUNTRY: USA  
ZIP: 10111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/195,705  
FILING DATE: 14-FEB-1994

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H  
REGISTRATION NUMBER: 32140  
REFERENCE/DOCKET NUMBER: 11880A3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-757-2200  
TELEFAX: 212-586-1461

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 394 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYDROTHERICAL: NO  
FRAGMENT TYPE: C-terminal

ORIGINAL SOURCE:  
ORGANISM: Plasmodium falciiparum  
STRAIN: MAD  
US-08-195-705-4

Query Match 92.8%; Score 1921; DB 2; Length 394;  
Best Local Similarity 98.4%; Pred. No. 1, 4e-137;  
Matches 368; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 18 AISTVTMDNLSGFENEYDVIYLLKPLAGVYRSLLKQIEKNIFTFNLNLDILNSRLKKRY 77  
Db 1 AISTVTMDNLSGFENEYDVIYLLKPLAGVYRSLLKQIEKNIFTFNLNLDILNSRLKKRY 60  
Qy 78 FLVDVLESDLMQFGHISSENEYIIDSFKLNSBQKNTLLSKYKIKESVENDIKFAQEGIS 137  
Db 61 FLVDVLESDLMQFGHISSENEYIIDSFKLNSBQKNTLLSKYKIKESVENDIKFAQEGIS 120  
Qy 138 YYEKVLAKYKDDLESIKKVIKEEKEKPPSSPPTTPPSPAKTDEOKKESKFLPFLTNITL 197  
Db 121 YYEKVLAKYKDDLESIKKVIKEEKEKPPSSPPTTPPSPAKTDEOKKESKFLPFLTNITL 180  
Qy 198 YNNLVNKIDYILNKKAKINDCNVEKDEAHVITKLSDLKALDIDKIDLFKNPYDEAIAI 257  
Db 181 YNNLVNKIDYILNKKAKINDCNVEKDEAHVITKLSDLKALDIDKIDLFKNHNDFAIAI 240  
Qy 258 LINDTKKDMGLKLGSTLVONFPNTIISKLEGFQDMNLSOHQCVKQCPENSGCFR 317  
Db 241 LINDTKKDMGLKLGSTLVONFPNTIISKLEGFQDMNLSOHQCVKQCPENSGCFR 300  
Qy 318 HLDREBECKCLNLYKQEGDKCVENPNPTCNENNGGCDADATCTBEDSGSSRKITCECTK 377  
Db 301 HLDREBECKCLNLYKQEGDKCVENPNPTCNENNGGCDADATCTBEDSGSSRKITCECTK 360

QY	378	PDSYPLFDGIFCSS	391
Db	361	PDSYPLFDGIFCSS	374

```

RESULT 11
US-09-500-376-3
; Sequence 3, Application US/09500376
; Patent No. 685316
; GENERAL INFORMATION:
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Baculovirus Produced Plasmodium falciparum Vaccine
; FILE REFERENCE: A-67984
; CURRENT APPLICATION NUMBER: US/09/500.376
; CURRENT FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: US 08/195,705
; PRIOR FILING DATE: 1994-02-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 394
; TYPE: PRT
; ORGANISM: plasmodium falciparum
; US-09-500-376-3

```

Query Match	92.8%	Score 1921;	DB 2;	Length 394;
Best Local Similarity	98.4%	Pred. No. 1.4e-137;		
Matches 368;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0

Qy	16	AISVTDNLISGSENEYDYLYKPLAGVYRS.LKKOIEKNI PFENLNDLINDLSRLKRRY	77
Db	1	AISVTDNLISGSENEYDYLYKPLAGVYRS.LKKOIEKNI ITFNLNDLINSRLKRRY	60
Qy	78	FLDVLSEDLMOFGHISSENEYIIEDSFKLNSBOKNTLLSKYKIKESYENDIKFAOBGIS	13
Db	61	FLDVLSEDLMOFGHISSENEYIIEDSFKLNSBOKNTLLSKYKIKESYENDIKFAOBGIS	120
Qy	138	YERKVLAKYKODLESIIKKVIEKEKEFPSSPTTPPSPAKTDOKKESKEPLFELTNIETL	197
Db	121	YERKVLAKYKODLESIIKKVIEKEKEFPSSPTTPPSPAKTDOKKESKEPLFELTNIETL	180
Qy	198	YNNLVNKIDYI.LNLAKINDCNEKDEAHVITITLSD.LKALDDKIDL.FKNPYPEALIKK	25
Db	181	YNNLVNKIDYI.LNLAKINDCNEKDEAHVITITLSD.LKALDDKIDL.FKNPYPEALIKK	240
Qy	258	LINDPTDKOMLGTLSGLVQNEPNTIISKLEIGKFOMLNISOHCYVKOCPENSGCFR	317
Db	241	LINDPTDKOMLGTLSGLVQIFPNTIISKLEIGKFOMLNISOHCYVKOCPENSGCFR	300
Qy	318	HLDBRECKCLINYYKQEGDKCVENPNTCENNNGGCDADATCTEEDSGSSRRKITTCECTK	377
Db	301	HLDBRECKCLINYYKQEGDKCENPNTCENNNGGCDADATCTEEDSGSSRRKITTCECTK	360
Qy	378	PDSYPLPFDGIFCSS 391	
Db	361	PDSYPLPFDGIFCSS 374	

RESULT 12  
US-09-117-415B-22  
Sequence 22, Application US/09117415B  
Patent No. 6551586  
GENERAL INFORMATION:  
APPLICANT: Davidson, Eugene  
Yang, Shurong  
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition  
of a MSAL Peptide  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE, PC  
STREET: 714 Colorado Avenue  
CITY: Bridgeport  
STATE: Connecticut

```

1      COUNTRY: USA
2      ZIP: 10017
3
4      COMPUTER READABLE FORM:
5      MEDIUM TYPE: floppy disk
6      COMPUTER: IBM PC compatible
7      OPERATING SYSTEM: PC-DOS/MS-DOS
8      SOFTWARE: wordpad (ASCII)
9
10     CURRENT APPLICATION DATA:
11     APPLICATION NUMBER: US/09/117,415B
12     FILING DATE: 29-Jul-1998
13
14     CLASSIFICATION: 435
15
16     ATTORNEY/AGENT INFORMATION:
17     NAME: Coleman, Henry D.
18     REGISTRATION NUMBER: 32,559
19     REFERENCE/DOCKET NUMBER: R12-030
20
21     TELECOMMUNICATION INFORMATION:
22     TELEPHONE: (212) 679-0090
23     TELEFAX: (212) 679-9121
24
25     INFORMATION FOR SEQ ID NO: 22:
26     SEQUENCE CHARACTERISTICS:
27     LENGTH: 613 amino acids
28     TYPE: amino acid
29     TOPOLOGY: linear
30
31     MOLECULE TYPE: protein
32     SEQUENCE DESCRIPTION: SEQ ID NO: 22:
33     US-09-117-415B-22

```

Query Match	56.3%	Score 1166.5	DB 2	Length 613
Best Local Similarity	58.0%	Pred. No. 3.6e-80		
Best Match 220, Conservative	55	Mismatches 83	Indels 21	Gaps 2

```

Oy 14 :GTMALSTVMONILSGFENEEDVLYIKRCLAGVRSLSKKOIEENIPTFMYLINDLINDLSRLK 73
Oy 253 TGEAVTBSVIDINILSKIENEYEVLYKPLAGVYLSLKOLENNVMTFVNVAKYDILNLSFEN 312
Oy 74 KRKYFLDVLDESJLMOFKHISISNEEYIIEDSFKLNSBOKNTLLSKSYKIKESVENDIKEAQ 133
Db 313 KRENFKVLBSDDLPHYDLTSSNVVVDPYKFLNKEKDKFLSSVNYIKDSIDTIDINFAN 372
Oy 134 EGISYIEYEKVLAKYDODDESICKVJKEEKKEKFPSSPPTTTPSPBAKTDEOKESKFLPFLTN 193
Db 373 DVLGYYYKILSEKYSKSDLDISICKYI-----NDKOGENEKMYLPFLDNL 412
Oy 194 IETLYNNLVNIDYILNLKAKINDCNVEKDEAHYKIKTFLSGLKAIIDKIDLFKXKPYOPE 253
Db 413 IETLYKYVNDKIDLFVJHLEAKVLNAVYIEKSNVEYKIKELNYLTKTIQDKLADFKONNFV 472
Oy 254 AIKKLINDTKDOMLKGKLSLTVL-ONEPNTIISKLEIGKQDOMLINISOHOCVKKOCPEN 312
Db 473 GIADLSIDTYNNHNNLLTKFLSTGMFENLAKTVYLSLIDGNOIGMGINISOHQCVKKOCPEN 532
Oy 313 SGCFRHLDEREECKCLLNYKOEGBKCVENPMPTCNENNGCCDADATCTIEBDSGSSRKKIT 372
Db 533 SGCFRHLDEREECKCLLNYKOEGBKCVENPMPTCNENNGCCDADAKCTEEDBSGSSNGKIT 592
Oy 373 CECTKPDSPYLPFDGIFCSS 391
Db 593 CECTKPDSPYLPFDGIFCSS 611

```

RESULT 13  
US-09-117-415B-18  
; Sequence 18, Application US/09117415B  
; Patent No. 6551586  
; GENERAL INFORMATION:  
; APPLICANT: Davidson, Eugene  
; Yang, Shulong  
; TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition  
; of a MSA1 Peptide  
; ;  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE, PC  
; STREET: 714 Colorado Avenue  
;

CITY: Bridgeport  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 10017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordpad (ASCII)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/117,415B  
FILING DATE: 29-Jul-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coleman, Henry D.  
REGISTRATION NUMBER: 32,559  
REFERENCE/DOCKET NUMBER: R12-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 679-9121  
TELEFAX: (212) 679-0090  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 631 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-117-415B-18

Query Match 56.3%; Score 1166.5; DB 2; Length 631;  
Best Local Similarity 58.0%; Pred. No. 3.7e-80;  
Matches 220; Conservative 55; Mismatches 83; Indels 21; Gaps 2;  
QY 14 SGTMAISTMTNIIISGFENEVDVYLKPLAGYRSLSKKQIEKNITFTPLNLDINSLK 73  
DB 271 TGEAVTPSVINDIILSKIENEYEVLYLKLPLAGYRSLSKKQLENNWTFVNVNVDILNSRFN 330  
QY 74 KRKYFLDVLSDLMQFKHIISSNEYIIEDSFKLLNSEOKNTLLSKYKIKESVENDIKFAQ 133  
DB 331 KRENKVNLESDDLIPYKDLTSSNYYVKDPYKFLNKEKDKFLSSYNYIKDSIDTDINRAN 390  
QY 134 EGI6EYEVKLYAKYKDDLESIKKVIKEKEKPPSPPTPPSPAKTDEOKESKFLPLTN 193  
DB 391 DVLGYIKLSKYSKSDLSIKKIYI-----NDKQGENEKYLPFLNN 430  
QY 194 IETLYNNLVNKIDVLYLNLKAKINDCNVEKQBAHYKITKLSDLKAIIDKIDLFKNPYPE 253  
DB 431 IETLYKTVNDKIDLFVHLKAKVNLVYIEKSNVEVKIKELNYLKTIDKLDLDFKQNNFV 490  
QY 254 AIKKLINDTKMDLQKGLSTGLV-QNFPNTIISKLIEGKFDMDLNIISOHCVKQCPEN 312  
DB 491 GIADLSTYNNHNLTKFLSTGMVFNENLAKTVLSLTLGMLNQGMLNISOHQCVKQCPON 550  
QY 313 SGCFRHLDEREECKCLNLYKQEGDKCVENPNTCNENNGGCDADATCTEEDSGSSRKKIT 372  
DB 551 SGCFRHLDEREECKCLNLYKQEGDKCVENPNTCNENNGGCDADAKCTEEDSGSGSKKIT 610  
QY 373 CECTKPDSPPLFDGIFCSS 391  
DB 611 CECTKPDSPPLFDGIFCSS 629

RESULT 14  
US-09-117-415B-20  
Sequence 20, Application US/09117415B  
Patent No. 6551586  
GENERAL INFORMATION:  
APPLICANT: Davidson, Eugene  
Yang, Shutong  
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition  
of a MSAL Peptide  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPHONE, PC  
STREET: 714 Colorado Avenue  
CITY: Bridgeport  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 10017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordpad (ASCII)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/117,415B  
FILING DATE: 29-Jul-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coleman, Henry D.  
REGISTRATION NUMBER: 32,559  
REFERENCE/DOCKET NUMBER: R12-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 679-0090  
TELEFAX: (212) 679-9121  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 631 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-117-415B-20

Query Match 56.3%; Score 1166.5; DB 2; Length 631;  
Best Local Similarity 58.0%; Pred. No. 3.7e-80;  
Matches 220; Conservative 55; Mismatches 83; Indels 21; Gaps 2;  
QY 14 SGTMAISTMTNIIISGFENEVDVYLKPLAGYRSLSKKQIEKNITFTPLNLDINSLK 73  
DB 253 TGEAVTPSVINDIILSKIENEYEVLYLKLPLAGYRSLSKKQLENNWTFVNVNVDILNSRFN 312  
QY 74 KRKYFLDVLSDLMQFKHIISSNEYIIEDSFKLLNSEOKNTLLSKYKIKESVENDIKFAQ 133  
DB 313 KRENKVNLESDDLIPYKDLTSSNYYVKDPYKFLNKEKDKFLSSYNYIKDSIDTDINRAN 372  
QY 134 EGI6EYEVKLYAKYKDDLESIKKVIKEKEKPPSPPTPPSPAKTDEOKESKFLPLTN 193  
DB 373 DVLGYIKLSKYSKSDLSIKKIYI-----NDKQGENEKYLPFLNN 412  
QY 194 IETLYNNLVNKIDVLYLNLKAKINDCNVEKQBAHYKITKLSDLKAIIDKIDLFKNPYPE 253  
DB 373 DVLGYIKLSKYSKSDLSIKKIYI-----NDKQGENEKYLPFLNN 412  
QY 194 IETLYNNLVNKIDVLYLNLKAKINDCNVEKQBAHYKITKLSDLKAIIDKIDLFKNPYPE 253  
DB 413 IETLYKTVNDKIDLFVHLKAKVNLVYIEKSNVEVKIKELNYLKTIDKLDLDFKQNNFV 472  
QY 254 AIKKLINDTKMDLQKGLSTGLV-QNFPNTIISKLIEGKFDMDLNIISOHCVKQCPEN 312  
DB 473 GIADLSTYNNHNLTKFLSTGMVFNENLAKTVLSLTLGMLNQGMLNISOHQCVKQCPON 532  
QY 313 SGCFRHLDEREECKCLNLYKQEGDKCVENPNTCNENNGGCDADATCTEEDSGSSRKKIT 372  
DB 533 SGCFRHLDEREECKCLNLYKQEGDKCVENPNTCNENNGGCDADAKCTEEDSGSGSKKIT 592  
QY 373 CECTKPDSPPLFDGIFCSS 391  
DB 593 CECTKPDSPPLFDGIFCSS 611

RESULT 15  
US-09-117-415B-16  
Sequence 16, Application US/09117415B  
Patent No. 6551586  
GENERAL INFORMATION:  
APPLICANT: Davidson, Eugene  
Yang, Shutong  
TITLE OF INVENTION: Malaria Vaccine Based Upon the Addition  
of a MSAL Peptide

```
/ NUMBER OF SEQUENCES: 24
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Henry D. Coleman, COLEMAN SUDOL SAPONE, PC
/ STREET: 714 Colorado Avenue
/ CITY: Bridgeport
/ STATE: Connecticut
/ COUNTRY: USA
/ ZIP: 10017
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPad (ASCII)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/117,415B
/ FILING DATE: 29-Jul-1998
/ CLASSIFICATION: 435
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coleman, Henry D.
/ REGISTRATION NUMBER: 32,559
/ REFERENCE/DOCKET NUMBER: R12-030
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 679-9121
/ TELEFAX: (212) 679-9121
/
/ INFORMATION FOR SEQ ID NO: 16:
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 649 amino acids
/ TYPE: amino acid
/ TOPOLOGY: 1linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 16:
/
/ US-09-117-415B-16

Query Match      56.3% Score 1166.5; DB 2; Length 649;
Best Local Similarity 58.0%; Pred No. 3,8e-80;
Matches 220; Conservative 55; Mismatches 83; Indels 21; Gaps 2;

QY 14 SGTMAISVTMDNISGFENEYDVIIYKPLAGVYRSLSKQIEKNIFTFNLINLINDIINSRLK 73
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 271 TGEAVTPSVINDIISKINENEYEVLYLKPLAGVYRSLSKQLENNVMTFNVNVADIINSRPN 330
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 74 KRKYLDVLESDFMOPKHISSNEIIEBSFKLLNSEOKNTLKSRYIKESVENDIKFAQ 133
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 331 KRENKVNLESDFLYKDLTSNYYVKDPYKFLNKEKDKFLSSYNYIKDSIDTDINPAN 390
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 134 EGISYEVKVLAKYKDDLESIKKVIKEBEKKFPSPPTTPSPAKTDEOKKESKFLPLTN 193
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 391 DVLGYIKTLEKIKSDLSIKKI-----NDKQGENEKYLPFLNN 430
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 194 IETLYNNLVNKIDVLYLNLKAKINDCNVEKDEAHVYKTKLSDLKAIIDKIDLFKNPYDFE 253
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 431 IETLYKTVNDKIDLVFIHLEAKVLNYYTEKSNEVEVKIKELNYLTKTIQDKLADFKANNFV 490
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 254 AIKKLIINDTKKDMGKLSLSTGLV-QNFPNTIISKLIEGKFQDMNLNISQHCVCYKQCPEN 312
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 491 GIADLSTYNNHNNLLTKFLSTGMVFNENLAKTVLSNLLDGNLQGMNLNISQHCVCYKQCPON 550
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 313 SGCPRHLDERECCKCLLVYKQBGDCVENPNPTCNENNGCCADATCTEEDSGSSRKKIT 372
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 551 SGCPRHLDERECCKCLLVYKQBGDCVENPNPTCNENNGCCADAKCTEEDSGSSRKKIT 610
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 373 CECTKPDGYPLFDGIFCSS 391
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 611 CECTKPDGYPLFDGIFCSS 629
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

Search completed: May 5, 2006, 00:26:11  
Job time : 48 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2006, 00:20:52 ; Search time 40 Seconds  
(without alignments)  
940.519 Million cell updates/sec

Title: US-10-057-532a-7  
Perfect score: 2071  
Sequence: 1 MAHHHHHGGSGSGTMAIS.....TCECTKPDSPYPLFDGFCSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%  
Maximum March 100%

Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1942	93.8	1701	2 A54498	major merozoite su
2	1931	93.2	1726	1 SRAQGM	major merozoite su
3	1921	92.8	1701	2 A26868	major merozoite su
4	1912.5	92.3	651	2 S47282	merozoite surface
5	1912	92.3	1726	2 A45948	major merozoite su
6	1166.5	56.3	400	2 A45545	major merozoite su
7	1166.5	56.3	1639	2 S05603	major merozoite su
8	1043	50.4	1631	1 SAZQK1	major merozoite su
9	1003	48.4	1640	2 A24594	probable major sur
10	792	38.2	1726	2 A39401	merozoite surface
11	781	37.7	1751	2 A45604	major blood-stage
12	553.5	26.7	680	2 A28121	major merozoite su
13	553.5	26.7	1772	2 A45532	major merozoite su
14	531	25.6	1785	2 A45546	major merozoite su
15	180.5	8.7	980	2 E71606	hypothetical prote
16	166	8.0	2166	2 G70163	hypothetical prote
17	160.5	7.7	1169	2 A64505	P115 homolog - Met
18	156.5	7.6	1939	2 T18372	repeat organellar
19	154	7.4	2269	2 T28677	rhodopy protein -
20	152	7.3	2401	2 T28676	rhodopy protein -
21	150	7.2	1156	2 B70356	chromosome assembl
22	149	7.2	1191	2 B97116	conserved hypotet
23	146	7.0	2819	2 A90551	hypothetical prote
24	145	7.0	1005	2 A64465	hypothetical prote
25	145	7.0	1130	2 T34081	hypothetical prote
26	144	7.0	1188	2 A71621	protein with 5'-3'
27	144	7.0	671	2 H64502	hypothetical prote
28	144	7.0	3394	2 T18501	hypothetical prote
29	143.5	6.9	1086	2 S16752	major merozoite su

30	143.5	6.9	1619	2 T18499	hypothetical prote
31	142.5	6.9	963	2 C90535	conserved hypotet
32	142	6.9	1187	2 T18355	hypothetical prote
33	140.5	6.8	819	2 E70105	P115 protein homol
34	140.5	6.8	864	2 B90395	purine NTPase [imp
35	140	6.8	1127	2 T28317	ORF MSY156 hypotet
36	140	6.8	1712	2 C71618	hypothetical prote
37	139.5	6.7	1979	2 C71622	hypothetical prote
38	139	6.7	652	2 B59102	hypothetical prote
39	138.5	6.7	624	2 PC6003	surface membrane p
40	138.5	6.7	2116	2 A26655	myosin heavy chain
41	138	6.7	442	2 T18507	hypothetical prote
42	137.5	6.6	909	2 C97325	hypothetical prote
43	137.5	6.6	1250	2 E81339	probable restricti
44	136	6.6	821	2 S67087	hypothetical prote
45	136	6.6	1163	2 G97236	ATPase involved in

ALIGNMENTS

RESULT 1  
A54498  
Major merozoite surface antigen precursor - 'malaria parasite (Plasmodium falciparum) (isc  
C:Species: Plasmodium falciparum  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 31-Dec-2004  
C:Accession: A54498

R:Peterson, M.G.; Coppel, R.L.; McIntyre, P.; Langford, C.J.; Woodrow, G.; Brown, G.V.; J  
Mol. Biochem. Parasitol. 27, 291-302, 1988  
A:Title: Variation in the precursor to the major merozoite surface antigens of Plasmodium  
A:Reference number: A54498; MUID:88142999; PMID:2449612  
A:Accession: A54498

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1701 <PRT>  
A:Cross-references: UNIPROT:P13819; UNIPARC:UPI000012F631; GB:M19143; NID:g160412; PIDN:f  
A:Superfamily: G surface protein  
C:Keywords: surface antigen

Query Match 93.8%; Score 1942; DB 2; Length 1701;

Best Local Similarity 99.2%; Ref. No. 1.2e-93;  
Matches 371; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	18	AISVTMDNIIISGFENEYVYIKPLAGVYRSKQIEKNIFTFNINLNDILNSRLKKRY	77
DB	1308	AISVTMDNIIISGFENEYVYIKPLAGVYRSKQIEKNITTFNINLNDILNSRLKKRY	1367
QY	78	FLDVLESPLMQFKHISSEYIIEDSFKLNSEQNTLKSYYIKESYENDIKFAQEGIS	137
DB	1368	FLDVLESPLMQFKHISSEYIIEDSFKLNSEQNTLKSYYIKESYENDIKFAQEGIS	1427
QY	138	YIEKYLAKYKDDLSIKVYIEEKKKPPSPPTTPPSAKTDEQKKSKFLPLTNITEL	197
DB	1428	YIEKYLAKYKDDLSIKVYIEEKKKPPSPPTTPPSAKTDEQKKSKFLPLTNITEL	1487
QY	198	YNNLVNKKIDVYLNLKAKINCNEKDEAHYIKRLSPDKAIDDKIDIDFKKPYDEAIKK	257
DB	1488	YNNLVNKKIDVYLNLKAKINCNEKDEAHYIKRLSPDKAIDDKIDIDFKKPYDEAIKK	1547
QY	258	LINDTKKMDLGLKLTGLVONFPNTIISKLIIEGKFDMLNISQHQYKQCPENSGCFR	317
DB	1548	LINDTKKMDLGLKLTGLVONFPNTIISKLIIEGKFDMLNISQHQYKQCPENSGCFR	1607
QY	318	HLDEREECKLANTKQBEDKVENPNPCNNNGCCADATCTEBDSSSSKKTICTECTK	377
DB	1608	HLDEREECKLANTKQBEDKVENPNPCNNNGCCADATCTEBDSSSSKKTICTECTK	1667
QY	378	PDSYPLFDGFCSS 391	
DB	1668	PDSYPLFDGFCSS 1681	

RESULT 2

SAZQM  
 major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (str  
 N:Alternate names: 195k glycoprotein  
 C:Species: Plasmodium falciparum  
 C>Date: 30-Sep-1987 #sequence\_revision 31-Mar-1991 #text\_change 31-Dec-2004  
 C:Accession: A26868; S06361  
 C:Accession: A26868; S06361  
 R:Weber, J.L.; Leininger, W.M.; Lyon, J.A.  
 Nucleic Acids Res. 14, 3311-3323, 1986  
 A:Title: Variation in the gene encoding a major merozoite surface antigen of the human m  
 A:Reference number: A23386; MUID:86205236; PMID:3517809  
 A:Accession: A23386  
 A:Molecule type: DNA  
 A:Residues: 1-1104 <WEB1>  
 A:Cross-references: UNIPROT:P04934; UNIPARC:UPI0000174696; EMBL:X03831  
 R:Weber, J.L.; Sim, B.K.L.; Lyon, J.A.; Wolff, R.  
 Nucleic Acids Res. 16, 1206, 1988  
 A:Title: Merozoite surface protein sequence from the Camp strain of the human malaria pa  
 A:Reference number: S06361; MUID:88143999; PMID:3278296  
 A:Accession: S06361  
 A:Molecule type: DNA  
 A:Residues: 1104-1726 <WEB2>  
 A:Cross-references: UNIPARC:UPI0000174697; EMBL:X03831  
 C:Comment: The merozoite stages of different strains have strain-specific surface antigen  
 C:Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The me  
 C:Superfamily: G surface protein  
 C:Keywords: glycoprotein; merozoite; surface antigen; tandem repeat  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-1726/Product: major merozoite surface antigen #status predicted <MAT>  
 F:67-87, 91-96, 100-105, 109-120/Region: 3-residue repeats (S-G-T)  
 F:757-765/Region: 3-residue repeats (T-E-E)  
 F:133, 272, 501, 567, 638, 827, 839, 924, 944, 990, 1016, 1114, 1221, 1613, 1658/Binding site: carbohy

Query Match 93.2%; Score 1931; DB 1; Length 1726;  
 Best Local Similarity 98.7%; Pred. No. 4, 7e-93;  
 Matches 369; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

18 AISTVMDNILSGFENEVDVYILKPLAGYRSILKKQIEKNITFTNLDILNSRLKKRY 77  
 DB 1333 AISTVMDNILSGFENEVDVYILKPLAGYRSILKKQIEKNITFTNLDILNSRLKKRY 1392  
 QY 78 FLDVLESQMLQPKHISNENYIIEDSFKLNSQKNTLKSYYIKESVENDIKFAQEGIS 137  
 DB 1393 FLDVLESQMLQPKHISNENYIIEDSFKLNSQKNTLKSYYIKESVENDIKFAQEGIS 1452  
 QY 138 YEKVLAKYKDDLESIKKYIKKEKKEFPSSPTTTPSPAKTDEQKESKFLPLTNIETL 197  
 DB 1453 YEKVLAKYKDDLESIKKYIKKEKKEFPSSPTTTPSPAKTDEQKESKFLPLTNIETL 1512  
 QY 198 YNNLVNKRIDDVILNKKAKINCNEKDEAHVKITKLSLKAIDDKIDLFKNPDPFAIKK 257  
 DB 1513 YNNLVNKRIDDVILNKKAKINCNEKDEAHVKITKLSLKAIDDKIDLFKNPDPFAIKK 1572  
 QY 258 LINDTKKMDLGLSTGLVONFPPTIISKLIEGFQDMLNISQHCYKQCPENSGCFR 317  
 DB 1573 LINDTKKMDLGLSTGLVONFPPTIISKLIEGFQDMLNISQHCYKQCPENSGCFR 1632  
 QY 318 HLDREBECKCLINLYKQEDKCEVNPPTCNENNGCCDADATCTBEDSSSKKTKTCECTK 377  
 DB 1693 HLDREBECKCLINLYKQEDKCEVNPPTCNENNGCCDADATCTBEDSSSKKTKTCECTK 1692  
 QY 378 PDSYPLPFGIFCSS 391  
 DB 1693 PDSYPLPFGIFCSS 1706

RESULT 3  
 A26868  
 major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (str  
 C:Species: Plasmodium falciparum  
 C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 31-Dec-2004  
 C:Accession: A26868  
 R:Tanabe, K.; Mackay, M.; Goman, M.; Scaife, J.G.  
 J. Mol. Biol. 195, 273-287, 1987

A:Title: Allelic dimorphism in a surface antigen gene of the malaria parasite Plasmodium  
 A:Reference number: A26868; MUID:88011243; PMID:3079521  
 A:Accession: A26868  
 A:Molecule type: DNA  
 A:Residues: 1-1701 <TAN>  
 A:Cross-references: UNIPARC:UPI000017778C  
 C:Superfamily: G surface protein  
 C:Keywords: surface antigen  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-1701/Product: major merozoite surface antigen #status predicted <MAT>

Query Match 92.8%; Score 1921; DB 2; Length 1701;  
 Best Local Similarity 98.4%; Pred. No. 1, 5e-92;  
 Matches 368; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

18 AISTVMDNILSGFENEVDVYILKPLAGYRSILKKQIEKNITFTNLDILNSRLKKRY 77  
 DB 1308 AISTVMDNILSGFENEVDVYILKPLAGYRSILKKQIEKNITFTNLDILNSRLKKRY 1367  
 QY 78 FLDVLESQMLQPKHISNENYIIEDSFKLNSQKNTLKSYYIKESVENDIKFAQEGIS 137  
 DB 1368 FLDVLESQMLQPKHISNENYIIEDSFKLNSQKNTLKSYYIKESVENDIKFAQEGIS 1427  
 QY 138 YEKVLAKYKDDLESIKKYIKKEKKEFPSSPTTTPSPAKTDEQKESKFLPLTNIETL 197  
 DB 1428 YEKVLAKYKDDLESIKKYIKKEKKEFPSSPTTTPSPAKTDEQKESKFLPLTNIETL 1487  
 QY 198 YNNLVNKRIDDVILNKKAKINCNEKDEAHVKITKLSLKAIDDKIDLFKNPDPFAIKK 257  
 DB 1488 YNNLVNKRIDDVILNKKAKINCNEKDEAHVKITKLSLKAIDDKIDLFKNPDPFAIKK 1547  
 QY 258 LINDTKKMDLGLSTGLVONFPPTIISKLIEGFQDMLNISQHCYKQCPENSGCFR 317  
 DB 1548 LINDTKKMDLGLSTGLVONFPPTIISKLIEGFQDMLNISQHCYKQCPENSGCFR 1607  
 QY 318 HLDREBECKCLINLYKQEDKCEVNPPTCNENNGCCDADATCTBEDSSSKKTKTCECTK 377  
 DB 1608 HLDREBECKCLINLYKQEDKCEVNPPTCNENNGCCDADATCTBEDSSSKKTKTCECTK 1667  
 QY 378 PDSYPLPFGIFCSS 391  
 DB 1668 PDSYPLPFGIFCSS 1681

RESULT 4  
 S47282  
 merozoite surface antigen 1 - malaria parasite (Plasmodium falciparum) (strain RO-71) (fr  
 C:Species: Plasmodium falciparum  
 A:Variety: strain RO-71  
 C>Date: 06-Jan-1995 #sequence\_revision 26-Jul-1996 #text\_change 31-Dec-2004  
 C:Accession: S47282  
 R:Tolle, R.; Bujard, H.; Cooper, J.A.  
 submitted to the EMBL Data Library, July 1994  
 A:Description: Plasmodium falciparum: recombination within the C-terminal region of mero  
 A:Reference number: S47282  
 A:Accession: S47282  
 A:Molecule type: DNA  
 A:Residues: 1-651 <TOL>  
 A:Cross-references: UNIPROT:Q25924; UNIPARC:UPI000008265F; EMBL:Z35329; NID:9535257; PID  
 A:Experimental source: strain RO-71  
 C:Superfamily: G surface protein  
 C:Keywords: glycoprotein; merozoite; surface antigen

Query Match 92.3%; Score 1912.5; DB 2; Length 651;  
 Best Local Similarity 98.1%; Pred. No. 1, 4e-92;  
 Matches 367; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

18 AISTVMDNILSGFENEVDVYILKPLAGYRSILKKQIEKNITFTNLDILNSRLKKRY 77  
 DB 259 AISTVMDNILSGFENEVDVYILKPLAGYRSILKKQIEKNITFTNLDILNSRLKKRY 318  
 QY 78 FLDVLESQMLQPKHISNENYIIEDSFKLNSQKNTLKSYYIKESVENDIKFAQEGIS 137

Db 319 FLVDLESDLMOFKHISSENYIIEDSFKLINSEOKNTLLSKYKIESVENDIKFAQEGIS 378  
QY 138 YEEKVLAKYKODLESIKKVIKEKEKPPSPPTTTPSPAKTDEOKKESKFLPLNINIEFL 197  
Db 379 YEEKVLAKYKODLESIKKVIKEKEKPPSPPTTTPSPAKTDEOKKESKFLPLNINIEFL 437  
QY 198 YNNLVNKIDVYLINLAKINDCNVEKDEAHVYKITYLSDLKAIIDDKIDLFKNPYDEAIKK 257  
Db 438 YNNLVNKIDVYLINLAKINDCNVEKDEAHVYKITYLSDLKAIIDDKIDLFKNHNDPEAIKK 497  
QY 258 LINDTCKDMIGKLIISTGLVONFPNTIISKLEIGKFDMLNISQHCYKQCPENSGCFR 317  
Db 498 LINDTCKDMIGKLIISTGLVONFPNTIISKLEIGKFDMLNISQHCYKQCPENSGCFR 557  
QY 318 HLDEREBCCLLNTYKQEGDKCVENPPTCNENNGGCDADATCTEEDSGSRKKITCECTK 377  
Db 558 HLDEREBCCLLNTYKQEGDKCVENPPTCNENNGGCDADAKTEEDSGSNGKKITCECTK 617  
QY 378 PDSYPLFDGIFCSS 391  
Db 618 PDSYPLFDGIFCSS 631

## RESULT 5

A45948  
major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (str  
C:Species: Plasmodium falciparum  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 31-Dec-2004  
C:Accession: A45948  
R:Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Case, S.E.; Siddiqui, W.A.  
Exp. Parasitol. 67, 1-11, 1988  
A:Title: Plasmodium falciparum: gene structure and hydrophathy profile of the major merozo  
A:Reference number: A45948; MUID:89005525; PMID:3049134  
A:Accession: A45948  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1726 <CNA>  
A:Cross-references: UNIPROT:Q25922; UNIPARC:UPI0000177F89; GB:M37213  
C:Superfamily: G surface protein  
C:Keywords: surface antigen

Query Match 92.3%; Score 1912; DB 2; Length 1726;  
Best Local Similarity 97.9%; Pred. No. 4.6e-92;  
Matches 366; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
QY 18 AISTYMNILISGFENEYDVILKPLAGYRSLSKKQIEKNITFTFNILNDILNSRLKKRY 77  
Db 1333 AISTYMNILISGFENEYDVILKPLAGYRSLSKKQIEKNITFTFNILNDILNSRLKKRY 1392  
QY 78 FLVDLESDLMOFKHISSENYIIEDSFKLINSEOKNTLLSKYKIESVENDIKFAQEGIS 137  
Db 1393 FLVDLESDLMOFKHISSENYIIEDSFKLINSEOKNTLLSKYKIESVENDIKFAQEGIS 1452  
QY 138 YEEKVLAKYKODLESIKKVIKEKEKPPSPPTTTPSPAKTDEOKKESKFLPLNINIEFL 197  
Db 1453 YEEKVLAKYKODLESIKKVIKEKEKPPSPPTTTPSPAKTDEOKKESKFLPLNINIEFL 1512  
QY 198 YNNLVNKIDVYLINLAKINDCNVEKDEAHVYKITYLSDLKAIIDDKIDLFKNPYDEAIKK 257  
Db 1513 YNNLVNKIDVYLINLAKINDCNVEKDEAHVYKITYLSDLKAIIDDKIDLFKNHNDPEAIKK 1572  
QY 258 LINDTCKDMIGKLIISTGLVONFPNTIISKLEIGKFDMLNISQHCYKQCPENSGCFR 317  
Db 1573 LINDTCKDMIGKLIISTGLVONFPNTIISKLEIGKFDMLNISQHCYKQCPENSGCFR 1632  
QY 318 HLDEREBCCLLNTYKQEGDKCVENPPTCNENNGGCDADATCTEEDSGSRKKITCECTK 377  
Db 1633 HLDEREBCCLLNTYKQEGDKCVENPPTCNENNGGCDADAKTEEDSGSNGKKITCECTK 1692  
QY 378 PDSYPLFDGIFCSS 391  
Db 1693 PDSYPLFDGIFCSS 1706

## RESULT 6

A45545  
major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (fragments)  
C:Species: Plasmodium falciparum  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 31-Dec-2004  
C:Accession: A45545  
R:Blackman, M.J.; Ling, I.T.; Nicholls, S.C.; Holder, A.A.  
Mol. Biochem. Parasitol. 49, 29-33, 1991  
A:Title: Proteolytic processing of the Plasmodium falciparum merozoite surface protein-1  
A:Reference number: A45545; MUID:92131048; PMID:1775158  
A:Accession: A45545  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-400 <BLA>  
A:Cross-references: UNIPROT:Q03999; UNIPARC:UPI000007B5E4  
A:Note: Sequence extracted from NCBI backbone (NCBI:77612, NCBI:77621)  
C:Superfamily: G surface protein  
C:Keywords: glycoprotein; merozoite; surface antigen; tandem repeat

Query Match 56.3%; Score 1166.5; DB 2; Length 400;  
Best Local Similarity 58.0%; Pred. No. 6.1e-54;  
Matches 220; Conservative 55; Mismatches 83; Indels 21; Gaps 2;

QY 14 SGTMAISTYMNILISGFENEYDVILKPLAGYRSLSKKQIEKNITFTFNILNDILNSRLK 73  
Db 22 TGEATPTVIDNINILSKINEYEVILKPLAGYRSLSKKQLENNWTFTVNVKXDLNSRPN 81  
QY 74 KRKYFLVDLESDLMOFKHISSENYIIEDSFKLINSEOKNTLLSKYKIESVENDIKFAQ 133  
Db 82 KRENFKNVLESDDLIPYKOLTSNNVVKQPYKFLNKEKDKFLSSYNIKDSIDTINPAN 141  
QY 134 EGISYEEKVLAKYKODLESIKKVIKEKEKPPSPPTTTPSPAKTDEOKKESKFLPLN 193  
Db 142 DVLGYKTLSEKYSDDLISIKYI-----NDKGENEKTILPLANN 181  
QY 194 IETLVNMLNKKIDVYLINLAKINDCNVEKDEAHVYKITYLSDLKAIIDDKIDLFKNPYDE 253  
Db 182 IETLVNMLNKKIDVYLINLAKINDCNVEKDEAHVYKITYLSDLKAIIDDKIDLFKNHNDPE 241  
QY 254 AIKVLINDTCKDMIGKLIISTGLVONFPNTIISKLEIGKFDMLNISQHCYKQCPEN 312  
Db 242 GIADLSTDYNNNNILTKFLSTGMVFNILAKTVLSNLDSNIGMLNISQHCYKQCPON 301  
QY 313 SCGRPHLDEREBCCLLNTYKQEGDKCVENPPTCNENNGGCDADATCTEEDSGSRKKIT 372  
Db 302 SCGRPHLDEREBCCLLNTYKQEGDKCVENPPTCNENNGGCDADAKTEEDSGSNGKKIT 361  
QY 373 CECTKPDYPLFDGIFCSS 391  
Db 362 CECTKPDYPLFDGIFCSS 380

## RESULT 7

S05603  
major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (str  
N:Alternate names: gp195 surface antigen  
C:Species: Plasmodium falciparum  
C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 31-Dec-2004  
C:Accession: S05603; S04850  
R:Myler, P.J.  
submitted to the EMBL Data Library, April 1989  
A:Reference number: S05603  
A:Accession: S05603  
A:Molecule type: mRNA  
A:Residues: 1-1639 <MYL>  
A:Cross-references: UNIPROT:P04933; UNIPARC:UPI000000672; EMBL:X15063; NID:99896; PIDN:C  
R:Myler, P.J.  
Nucleic Acids Res. 17, 5401, 1989  
A:Title: Nucleotide and deduced amino acid sequence of the gp195 (MSA-1) gene from plasm  
A:Reference number: S04850; MUID:89345116; PMID:2668887  
A:Accession: S04850  
A:Molecule type: mRNA





## RESULT 10

A39401

merozoite surface antigen 1 precursor - Plasmodium vivax

C:Species: Plasmodium vivax

C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 31-Dec-2004

C:Accession: A39401

Ridel Portillo, H.A.; Longacre, S.; Khouri, E.; David, P.H.

Proc. Natl. Acad. Sci. U.S.A. 88, 4030-4034, 1991

A:Title: Primary structure of the merozoite surface antigen 1 of Plasmodium vivax reveal

A:Reference number: A39401; MUID:91219506; PMID:2023952

A:Accession: A39401

A:Status: Preliminary

A:Molecule type: DNA

A:Cross-references: UNIPROT:Q02569; UNIPARC:UPI0000177F98; GB:M60807

C:Superfamily: G surface protein

C:Keywords: surface antigen

Query Match 38.2%; Score 792; DB 2; Length 1726;

Best Local Similarity 43.1%; Pred. No. 1,le-33;

Matches 160; Conservative 75; Mismatches 114; Indels 22; Gaps 7;

QY 32 NEVDYIYKPLAGVRSLSKKQIEKNIPTFNILNDILNSRLKKRYFLDVLSDLMQPKH 91

DB 1346 SDYDVVYIKPLAGMYKIKKQLEHNHVAFNNTITDMLDSRLKKRYFLEVLNSDLNPFXY 1405

QY 92 ISSNEYIIEDSFKLNSQKNTLKSYYKIKESVENDIKFAQEGISYYEKLAKYKDDL- 150

DB 1406 SPGSGYIIKDPYKLLDLKKKLLGSKYKIGASIDKIDGTANDGVNYYNKGELYKTHLT 1465

QY 151 ---ESIKKY---IKSEKKEFPSPPTTPSPAKTDEOKKES---KFLPFLTNIETLYNNLT 201

DB 1466 AVNEEVKAYVEADIKAEEDKIKIGSDSTTKTETSMAKKALEKILPFLNLSQKYESL 1525

QY 202 VNKIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYPFAIKKLIND 261

DB 1526 VSKVNTYTDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK---KSEKK--NE 1578

QY 262 DTKDMLKGLSTGLV-QNFPNTIISKLEGFQDMLNISQCYKCKQCPENSGCFRHL 320

DB 1579 VKSGLTEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPVDMNAACYRYLD 1638

QY 321 ERECKCCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRKIRICECTKPD 380

DB 1639 GMEERKCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---NKIVCKCTKES 1694

QY 381 YLPFDGIFCSS 391

DB 1695 EPLFEGVFCSS 1705

QY 151 ---ESIKKY---IKSEKKEFPSPPTTPSPAKTDEOKKES---KFLPFLTNIETLYNNLT 201

DB 1466 AVNEEVKAYVEADIKAEEDKIKIGSDSTTKTETSMAKKALEKILPFLNLSQKYESL 1525

QY 202 VNKIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYPFAIKKLIND 261

DB 1526 VSKVNTYTDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK---KSEKK--NE 1578

QY 262 DTKDMLKGLSTGLV-QNFPNTIISKLEGFQDMLNISQCYKCKQCPENSGCFRHL 320

DB 1579 VKSGLTEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPVDMNAACYRYLD 1638

QY 321 ERECKCCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRKIRICECTKPD 380

DB 1639 GMEERKCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---NKIVCKCTKES 1694

QY 381 YLPFDGIFCSS 391

DB 1695 EPLFEGVFCSS 1705

QY 151 ---ESIKKY---IKSEKKEFPSPPTTPSPAKTDEOKKES---KFLPFLTNIETLYNNLT 201

DB 1466 AVNEEVKAYVEADIKAEEDKIKIGSDSTTKTETSMAKKALEKILPFLNLSQKYESL 1525

QY 202 VNKIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYPFAIKKLIND 261

DB 1526 VSKVNTYTDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK---KSEKK--NE 1578

QY 262 DTKDMLKGLSTGLV-QNFPNTIISKLEGFQDMLNISQCYKCKQCPENSGCFRHL 320

DB 1579 VKSGLTEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPVDMNAACYRYLD 1638

QY 321 ERECKCCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRKIRICECTKPD 380

DB 1639 GMEERKCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---NKIVCKCTKES 1694

QY 381 YLPFDGIFCSS 391

DB 1695 EPLFEGVFCSS 1705

QY 151 ---ESIKKY---IKSEKKEFPSPPTTPSPAKTDEOKKES---KFLPFLTNIETLYNNLT 201

DB 1466 AVNEEVKAYVEADIKAEEDKIKIGSDSTTKTETSMAKKALEKILPFLNLSQKYESL 1525

QY 202 VNKIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYPFAIKKLIND 261

DB 1526 VSKVNTYTDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK---KSEKK--NE 1578

QY 262 DTKDMLKGLSTGLV-QNFPNTIISKLEGFQDMLNISQCYKCKQCPENSGCFRHL 320

DB 1579 VKSGLTEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPVDMNAACYRYLD 1638

QY 321 ERECKCCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRKIRICECTKPD 380

DB 1639 GMEERKCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---NKIVCKCTKES 1694

QY 381 YLPFDGIFCSS 391

DB 1695 EPLFEGVFCSS 1705

QY 151 ---ESIKKY---IKSEKKEFPSPPTTPSPAKTDEOKKES---KFLPFLTNIETLYNNLT 201

DB 1466 AVNEEVKAYVEADIKAEEDKIKIGSDSTTKTETSMAKKALEKILPFLNLSQKYESL 1525

QY 202 VNKIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYPFAIKKLIND 261

DB 1526 VSKVNTYTDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK---KSEKK--NE 1578

QY 262 DTKDMLKGLSTGLV-QNFPNTIISKLEGFQDMLNISQCYKCKQCPENSGCFRHL 320

DB 1579 VKSGLTEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPVDMNAACYRYLD 1638

QY 321 ERECKCCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRKIRICECTKPD 380

DB 1639 GMEERKCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---NKIVCKCTKES 1694

Matches 156; Conservative 78; Mismatches 104; Indels 44; Gaps 6;

QY 32 NEVDYIYKPLAGVRSLSKKQIEKNIPTFNILNDILNSRLKKRYFLDVLSDLMQPKH 91

DB 1371 SDYDVVYIKPLAGMYKIKKQLEHNHVAFNNTITDMLDSRLKKRYFLEVLNSDLNPFXY 1430

QY 92 ISSNEYIIEDSFKLNSQKNTLKSYYKIKESVENDIKFAQEGISYYEKLAKYKDDL 151

DB 1431 SSSGSGYIIKDPYKLLDLKKKKLLISYYKIGASIDMLATANDGYVYNNKGELYKTHLD 1490

QY 152 SIKYIKSEKKEFPSPPTTPSPAKTDEOKKE-----SKFLPF 190

DB 1491 GWKTEIKKVEDDI-----KKQDEELKGNVNSODSKNEFLAKKALEKILPFL 1539

QY 191 LTNIEFLNLYNKNIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYP 250

DB 1540 LNSLQKYESLSVSKVNTITDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK--- 1596

QY 251 DFEAIKKLINDTKKMDLGLSTGLV-QNFPNTIISKLEGFQDMLNISQHCYKQC 309

DB 1597 ---KSEKK--NEVKSGLLEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPV 1652

QY 310 PENSGCFRHLDERECKCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRK 369

DB 1653 PDNAACYRYLDGTBEERCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---N 1708

QY 370 KITCECTKPDYLPFDGIFCSS 391

DB 1709 KIVCKCTKESGEPLEFEGVFCSS 1730

QY 151 ---ESIKKY---IKSEKKEFPSPPTTPSPAKTDEOKKES---KFLPFLTNIETLYNNLT 201

DB 1466 AVNEEVKAYVEADIKAEEDKIKIGSDSTTKTETSMAKKALEKILPFLNLSQKYESL 1525

QY 202 VNKIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYPFAIKKLIND 261

DB 1526 VSKVNTYTDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK---KSEKK--NE 1578

QY 262 DTKDMLKGLSTGLV-QNFPNTIISKLEGFQDMLNISQCYKCKQCPENSGCFRHL 320

DB 1579 VKSGLTEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPVDMNAACYRYLD 1638

QY 321 ERECKCCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRKIRICECTKPD 380

DB 1639 GMEERKCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---NKIVCKCTKES 1694

QY 381 YLPFDGIFCSS 391

DB 1695 EPLFEGVFCSS 1705

QY 151 ---ESIKKY---IKSEKKEFPSPPTTPSPAKTDEOKKES---KFLPFLTNIETLYNNLT 201

DB 1466 AVNEEVKAYVEADIKAEEDKIKIGSDSTTKTETSMAKKALEKILPFLNLSQKYESL 1525

QY 202 VNKIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYPFAIKKLIND 261

DB 1526 VSKVNTYTDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK---KSEKK--NE 1578

QY 262 DTKDMLKGLSTGLV-QNFPNTIISKLEGFQDMLNISQCYKCKQCPENSGCFRHL 320

DB 1579 VKSGLTEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPVDMNAACYRYLD 1638

QY 321 ERECKCCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRKIRICECTKPD 380

DB 1639 GMEERKCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---NKIVCKCTKES 1694

QY 381 YLPFDGIFCSS 391

DB 1695 EPLFEGVFCSS 1705

QY 151 ---ESIKKY---IKSEKKEFPSPPTTPSPAKTDEOKKES---KFLPFLTNIETLYNNLT 201

DB 1466 AVNEEVKAYVEADIKAEEDKIKIGSDSTTKTETSMAKKALEKILPFLNLSQKYESL 1525

QY 202 VNKIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYPFAIKKLIND 261

DB 1526 VSKVNTYTDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK---KSEKK--NE 1578

QY 262 DTKDMLKGLSTGLV-QNFPNTIISKLEGFQDMLNISQCYKCKQCPENSGCFRHL 320

DB 1579 VKSGLTEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPVDMNAACYRYLD 1638

QY 321 ERECKCCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRKIRICECTKPD 380

DB 1639 GMEERKCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---NKIVCKCTKES 1694

QY 381 YLPFDGIFCSS 391

DB 1695 EPLFEGVFCSS 1705

QY 151 ---ESIKKY---IKSEKKEFPSPPTTPSPAKTDEOKKES---KFLPFLTNIETLYNNLT 201

DB 1466 AVNEEVKAYVEADIKAEEDKIKIGSDSTTKTETSMAKKALEKILPFLNLSQKYESL 1525

QY 202 VNKIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYPFAIKKLIND 261

DB 1526 VSKVNTYTDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK---KSEKK--NE 1578

QY 262 DTKDMLKGLSTGLV-QNFPNTIISKLEGFQDMLNISQCYKCKQCPENSGCFRHL 320

DB 1579 VKSGLTEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPVDMNAACYRYLD 1638

QY 321 ERECKCCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRKIRICECTKPD 380

DB 1639 GMEERKCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---NKIVCKCTKES 1694

QY 381 YLPFDGIFCSS 391

DB 1695 EPLFEGVFCSS 1705

QY 151 ---ESIKKY---IKSEKKEFPSPPTTPSPAKTDEOKKES---KFLPFLTNIETLYNNLT 201

DB 1466 AVNEEVKAYVEADIKAEEDKIKIGSDSTTKTETSMAKKALEKILPFLNLSQKYESL 1525

QY 202 VNKIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYPFAIKKLIND 261

DB 1526 VSKVNTYTDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK---KSEKK--NE 1578

QY 262 DTKDMLKGLSTGLV-QNFPNTIISKLEGFQDMLNISQCYKCKQCPENSGCFRHL 320

DB 1579 VKSGLTEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPVDMNAACYRYLD 1638

QY 321 ERECKCCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRKIRICECTKPD 380

DB 1639 GMEERKCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---NKIVCKCTKES 1694

QY 381 YLPFDGIFCSS 391

DB 1695 EPLFEGVFCSS 1705

QY 151 ---ESIKKY---IKSEKKEFPSPPTTPSPAKTDEOKKES---KFLPFLTNIETLYNNLT 201

DB 1466 AVNEEVKAYVEADIKAEEDKIKIGSDSTTKTETSMAKKALEKILPFLNLSQKYESL 1525

QY 202 VNKIDYIYLNKAKINDCNVEKDEAHVKITKLSDKAIDKIDLPKPNYPFAIKKLIND 261

DB 1526 VSKVNTYTDNLKAVINNCQLEKKEAEITVKKLQDYNNKDEKLEKYK---KSEKK--NE 1578

QY 262 DTKDMLKGLSTGLV-QNFPNTIISKLEGFQDMLNISQCYKCKQCPENSGCFRHL 320

DB 1579 VKSGLTEKLMKSKIKIKENSKIELISOLLNVQTLTMSSEHTCIDTNPVDMNAACYRYLD 1638

QY 321 ERECKCCLNLYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRKIRICECTKPD 380

DB 1639 GMEERKCLTTFKEBEGKCVPSNVTCKDNGGCAPEAECKMTDS---NKIVCKCTKES 1694

QY 381 YLPFDGIFCSS 391

```

Qy 282 NTIISKLEGRFOMLNI-S-OHCV-KKQCEPNSGCFPHLDERECCKLLANYK-EGDKC 338
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 548 KKLIAKMLNMDGMDLLGVDPKHVCYDRDIPKNAACCFRFDGTEBWRCLLGIKKGEINTC 607

Qy 339 VENNPTCNENNNGGCDADATCTEEDSGSSRKKTITECTKPDSPYLPFDGIFCSS 391
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 608 VENNPTCDINNNGGCDPTASCONAESTENSKKIIITCTCKEPTPNAYYEGVFCSS 660

RESULT 13
A45532
major mezozoite surface antigen precursor - Plasmodium yoelii
CISpecies: Plasmodium yoelii
CISDate: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 31-Dec-2004
CISAccession: A45532; A45531
RILewis, A.P.
Mol. Biochem. Parasitol. 36, 271-282, 1989
A:Title: Cloning and analysis of the gene encoding the 230-kilodalton mezozoite surface
A:Reference number: A45532; MUID:90014981; PMID:2797063
A:Accession: A45532
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1772 <LEM>
A:Cross-references: UNIPROT:P13828; UNIPARC:UPI000012F636; GB:J04666; NID:g160492; PID:g
R.Daly, T.M.; Burns Jr., J.M.; Long, C.A.
Mol. Biochem. Parasitol. 36, 283-285, 1989
A:Title: Precursor to the major mezozoite surface antigen of Plasmodium yoelii: cloning
A:Reference number: A45531; MUID:90014982; PMID:2797064
A:Accession: A45531
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 454-1094 <DAL>
A:Cross-references: UNIPARC:UPI0000000390; GB:J03975; NID:g160081; PID:g160082
A:Superfamily: G surface protein
C:Keywords: surface antigen

Query Match 26.7%; Score 553.5; DB 2; Length 1772;
Best Local Similarity 30.8%; Pred. No.3,1e-21;
Matches 127; Conservative 88; Mismatches 147; Indels 51; Gaps 9;

Qy 9 PG--GSGSGTMAISVTMD-----NIIISGENEDVIYLKPLAG 44
Db 1361 PGAVPGSGTDRVAGSSVDNEDDIYQIASGSEDAPEKDIISBFTNESLYVYTKRLGS 1420

Qy 45 VYRGLKQIOEKNIPTFNINLNDILNSRLKRRKRYFLDVEESDLMQFKHISNEYIIEBSFK 104
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1421 TYKRLKGMLEPFSTIKEDMTNGLNNKSQKNDPLEVLSHSLDLFKDSTLKVIYIRNPQ 1480

Qy 105 LLNSEEOKTLLSKSYKIESYENDIKFAOEGISYEVKVLAKYKDDLESIKVIEKEKEK 164
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1481 LLDDNDKDKQIVNLKYAKRKGINEDIETTDGKFPNNKMWELYNQGLAAVGEQIATIE--- 1537

Qy 165 PSSPPTTPPSPAKTEDEQKE--SKFLPPLNIEFLYNLVNKIDYILNFAKINDCNVE 222
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1538 -----AETNDTKEEKKKYIPILEDLKGLEYIVIGQAEYSSEHLQNRLDNYKNE 1586

Qy 223 KDEAHVKTITKLSDLKADIDKIDFLGNPYDFFAIKKLINLDITKMKMLGKLTSLGV-QNPF 281
1587 KAEPEILTKNLEKXIODEKDEFEYHAE-----NKKHIASIALNNLNKSGLVGEGS 1639

Qy 282 NTIISKLEGRFOMLNI-S-OHCV-KKQCEPNSGCFPHLDERECCKLLANYK-EGDKC 338
Db 1640 KKLIAKMLNMDGMDLLGVDPKHVCYDRDIPKNAACCFRFDGTEBWRCLLGIKKGEINTC 1699

Qy 339 VENNPTCNENNNGGCDADATCTEEDSGSSRKKTITECTKPDSPYLPFDGIFCSS 391
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1700 VENNPTCDINNNGGCDPTASCONAESTENSKKIIITCTCKEPTPNAYYEGVFCSS 1752

RESULT 14
A45546
major mezozoite surface antigen precursor - Plasmodium chabaudi chabaudi

```

C:Species: Plasmodium chabaudi  
C.Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 31-Dec-2004

C.Accession: A45546  
R.Deleerijder, W.; Hendrix, D.; Bendaïman, N.; Hanegreels, J.; Brijs, L.; Hamers-Casteren M.L. Biochem. Parasitol. 43, 231-244, 1990  
A>Title: Molecular cloning and sequence analysis of the gene encoding the major merozoite surface protein p85.  
A.Reference number: A45546; PMID:51218805; PMID:2090945  
A.Accession: A45546  
A.Status: Preliminary  
A.Molecule type: mRNA  
A.Residues: 1-1785 <DEL>  
A.Cross-references: UNIPROT:Q25685; UNIPARC:UPI000007B6DB; GB:M34947; MID:g160597; PID:g160597  
C.Keywords: G surface protein  
Keywords: Surface antigen

Query Match      25.6%; Score 531; DB 2; Length 1785;  
Best Local Similarity    32.4%; Pred. No. 4,6e-20;  
Matches     122; Conservative       86; Mismatches    134; Indels    34; Gaps    11;

Dy                  25 NILSFEENEYDIYLKPLAGVTRSLKKQIEKIIFTNLNDI---LSNLRKRKYFLDV    81  
Dd                  1415 ILDAFKSENEEYITRKSLGNTTKSPFGMLKE--FSMIEDIMTGLNYLEKKNDFLDV    1471  
  
Oy                  82 LESDMOFKHISSENXYEDSFRLNSBOOKTLTKVKYIKESVDNIKFPADEGISYYEK    141  
Db                  1472 LSYLEALFFDDINTNFVNVPYQLDNDRKKDKMTLKRAIKGVTEIDETATDIGIEFPNK    1531  
  
Oy                  142 VLAKYKDLESISKVIKEKERFPPSSPTTPPSAPKTDEOKSKELPFLTINIELLYNLT    201  
Db                  1532 MIELYKPQNANVEGI-----AAIGTER-----TDAREK-KVAPIREDLGIVETI    1576  
  
Oy                  202 VNKIDDYILNLKAANKDCNVGEDEAHVTITKSCLKAIIDKIDLFNKPYPEAFIAKLIND    261  
Db                  1577 LNGAEEFBELLQHKKENYEIKEAGFDLMANTTYIRIDEKEDF----VESAEK-NK    1629  
  
Oy                  262 DTCKMDLKGILTSTGY-QNPFTTIISKLIEGRFODMI-L-SHQCVKQGCPENSACPRHL    319  
Db                  1630 HIASIALNNLNKSGVLTBESKKILLAKMLMDAMDLLTGGSNHVCISTPDPNAKCRRYD    1689  
  
Oy                  320 DERBECKCLANYKO--EGDKCYENPNPTCNENNNGCCADATCTBEDS--GSRKKRTCEC    375  
Db                  1690 DGTEEMRCILGFMRKXODPDGNCRCAADDAPVCNMNNGGCCDXAADCEVENTBDPSKKIVCTC    1749  
  
Oy                  376 TKPDSYPLEFDGFCSS    391  
Db                  1750 KEPNNAYAVGVFCSS    1765

RESULT 15

E71606 Hypochemical protein PFB0765w - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C>Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 31-Dec-2004  
C.Accession: E71606  
R.Gardner, M.J.; Icttelin, H.; Carnucci, D.J.; Cummings, L.M.; Araavind, L.; Koonin, E.V.; Partee, M.I.; Salberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O., et al. Science 282, 1126-1132, 1998  
A>Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A.Reference number: A71600; PMID:99021743; PMID:9804551  
A.Accession: E71606  
A>Status: Preliminary; nucleic acid sequence not shown; translation not shown  
A.Molecule type: DNA  
A.Residues: 1-980 <GAR>  
A.Cross-references: UNIPROT:O81659; UNIPARC:UPI00001788FI; GB:AEO01417; GB:AEO01362; MID:  
A.Experimental source: clone 3D7  
C.GeneticSB  
A:Gene: PFB0765w

Query Match      8.7%; Score 180.5; DB 2; Length 980;  
Best Local Similarity    23.7%; Pred. No. 0.043;  
Matches     102; Conservative       77; Mismatches    140; Indels    11; Gaps    23;

31 ENEDVITYLKPLAGVRSLKKQIEKNI-----FTTNLNDI---NSRLKK    74

```

Dd      : | | |||          : |||||         :   : | || : : || : |
2t8 QNYT---YHK--EYDLKQKELEKNIEHGKLEHLSHCYEENOKLNEI KARNSTIKN 301

Qy      75 RKYFLDLV---ESDLMQPHIS-----SNEYIID-----SFK 104t
       : | : | : | : | : | : | : | : | : | : | : | : | : | : |
3o2 KORXIDLLTNINELLKKKEINNIIKLMEKONVIKNNQGLDKIDENEKNGEHVNKLQNE 361t

Oy      1o5 LINSQKNTLL-KSYTYITESVENDIKPAQEGISTYEKVLAKYKDDESIK-----155S
       : | : | : | : | : | : | : | : | : | : | : | : | : | : |
3e2 LIKRELONNCICKRDI EFCCKEKEDKJKNJEDDLLKCKCIENLKDELINTIKKQMEDBM 421t

Oy      156 -----VINEKEXFPESPPTTPPSPAKTBEQ-----KKESFBLPFTNIETLV-NLVNKI 2o5t
       : : : : : : : : : : : : : | : | : | : | : | : | : | : |
422 TNEMDLLSKVEBELNRINKTYEKNAVIELNNELDVIRKKLNDEFLEEEKKKOIDMYKI 4e1t

Oy      2o6 DYLINLKAINDC-NVEKDEAHVKITKLSDLKAIDDKIDLFGNPYPFEAIKKLINDTK 2e4t
       : : : : : : : : : : : : : | : | : | : | : | : | : | : |
4e2 KEYELOIKENEKEIBDSLKNGEQNLHVLYKNBEL---NEKEILIKNKXDK-E INMIIEQYNK 557t

Oy      2e5 ----KDMIGKLLSGTLGVNPFVTIISKLIBGKFQ-----DMNISOHOCVFKCPPE 311t
       : ||||| : | : | : | : | : | : | : | : | : | : | : |
538 KIOEBKMDMLNNIKKS-MDQTHKQJEBMOEBENKKEKLRUKNVCDM- NLQSOLIK----E 591t

Oy      312 NSGCRRHLDER-BECKCLANVK-----QBBDKVBNPNPCFNENNNGCCDADATCEE 3e2t
       : : : : : : : : : : : : : | : | : | : | : | : | : | : |
592 NE---KHMOEKVEEYKNLLKORDQBELKONIIOBYDERIEIONKEMEDIIVNDCEBKL-----K 644t
       : : : : : : : : : : : : : | : | : | : | : | : | : | : |

Oy      3e3 DGSSRKKIT 372
       : : : : : | : | : | : | : | : | : | : | : | : | : |
645 OAKINNKULT 654

```

Search completed: May 5, 2006, 00:25:18  
Job time : 41 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2006, 00:17:57 ; Search time 231 Seconds  
(without alignments)  
1194.206 Million cell updates/sec

Title: US-10-057-532a-7  
Perfect score: 2071  
Sequence: 1 MAHHHHHPPGGSGGTMAIS.....TCECTKPDPYPLDFGIFCSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1965	94.9	1720	2	Q25922_PLAFA
2	1965	94.9	1720	2	Q25922_PLAFA
3	1961	94.7	652	2	Q25923_PLAFA
4	1942	93.8	373	2	Q25723_PLAFA
5	1942	93.8	570	2	Q25972_PLAFA
6	1942	93.8	570	2	Q25968_PLAFA
7	1942	93.8	1694	2	Q25968_PLAFA
8	1942	93.8	1701	1	MSPI_PLAFA
9	1942	93.8	1701	1	MSPI_PLAFA
10	1935	93.4	373	2	Q25722_PLAFA
11	1933	93.3	373	2	Q25722_PLAFA
12	1932.5	93.3	569	2	Q25978_PLAFA
13	1931	93.2	1726	1	MSPI_PLAFA
14	1930.5	93.2	1682	1	MSPI_PLAFA
15	1929	93.1	373	2	Q25922_PLAFA
16	1928	93.1	1726	1	MSPI_PLAFA
17	1928	93.1	1726	1	MSPI_PLAFA
18	1926.5	93.0	569	2	Q25980_PLAFA
19	1926.5	93.0	569	2	Q25970_PLAFA
20	1926.5	93.0	569	2	Q25982_PLAFA
21	1926.5	93.0	1688	2	Q25982_PLAFA
22	1926.5	93.0	1700	2	Q25982_PLAFA
23	1924	92.9	373	2	Q25724_PLAFA
24	1922.5	92.8	372	2	Q25717_PLAFA
25	1919	92.7	373	2	Q25721_PLAFA
26	1919	92.7	373	2	Q25995_PLAFA
27	1917.5	92.6	372	2	Q25718_PLAFA
28	1917.5	92.6	372	2	Q25718_PLAFA
29	1917.5	92.6	372	2	Q25720_PLAFA
30	1917	92.6	1689	2	Q25720_PLAFA
31	1916.5	92.5	569	2	Q25983_PLAFA

32	1912.5	92.3	651	2	Q25924_PLAFA
33	1910.5	92.3	569	2	Q25975_PLAFA
34	1910.5	92.3	569	2	Q25974_PLAFA
35	1910.5	92.3	569	2	Q25979_PLAFA
36	1910.5	92.3	569	2	Q25977_PLAFA
37	1910.5	92.3	569	2	Q25969_PLAFA
38	1910.5	92.3	1688	2	Q25969_PLAFA
39	1910.5	92.3	1688	2	Q25969_PLAFA
40	1910.5	92.3	1694	2	Q25969_PLAFA
41	1910.5	92.3	1699	2	Q25969_PLAFA
42	1910.5	92.3	1704	2	Q25969_PLAFA
43	1906.5	92.1	372	2	Q25725_PLAFA
44	1901.5	91.8	372	2	Q25726_PLAFA
45	1900.5	91.8	372	2	Q25997_PLAFA

ALIGNMENTS

RESULT 1					
ID	Q25922_PLAFA	PRELIMINARY;	PRT;	1720 AA.	
AC	Q25922;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Precursor of the major mezoite surface antigens precursor.				
GN	Name=gp190/MSAI/MSPI/PMMSA;				
OS	Plasmodium falciparum.				
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				
OX	NCBI_TaxID=5833;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=NF54;				
RX	MEDLINE=95354793; PubMed=7628566; DOI=10.1006/expr.1995.1091;				
RA	Tolle R., Bujard H., Cooper J.A.;				
RT	"Plasmodium falciparum: Variations within the C-terminal region of mezoite surface antigen-1.";				
RL	Exp. Parasitol. 81:47-54(1995).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=NF54;				
RX	MEDLINE=96123395; PubMed=8577332; DOI=10.1016/0166-6851(95)00094-H;				
RA	Pan W., Tolle R., Bujard H.;				
RT	"A direct and rapid sequencing strategy for the Plasmodium falciparum antigen gene gp190/MSAI.";				
RL	Mol. Biochem. Parasitol. 73:241-244(1995).				
CC	-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).				
DR	EMBL; Z35327; CA84556.1; -; Genomic_DNA.				
DR	PIR; A45948; A45948.				
DR	HSSP; P04933; ICBJ.				
DR	SMR; Q25922; 1607-1699.				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	GO; GO:0009405; P:pathogenesis; IEA.				
DR	InterPro; IPR006209; EGF like.				
DR	InterPro; IPR010901; MSPI_C.				
DR	Pfam; PF00008; EGF_1.				
DR	Pfam; PF07462; MSPI_C; 1.				
KW	Membrane; Mezoite; Repeat; Signal.				
FT	SIGNAL 1 19 Potential.				
SQ	SEQUENCE 1720 AA; 195727 MW; 717B2FD1B637AB83 CRC64;				
Query Match 94.9%; Score 1965; DB 2; Length 1720;					
Best Local Similarity 100.0%; Pred. No. 1.3e-90; Indels 0; Gaps 0;					
Matches 374; Conservative 0; Mismatches 0;					
Qy	18 AISTVMDIISGFENEVDVYIKPLAGYVRSLKKQIEKNIETPNLNDLINSRLKKRY 77				
Db	1327 AISTVMDIISGFENEVDVYIKPLAGYVRSLKKQIEKNIETPNLNDLINSRLKKRY 1386				
Qy	78 FLVDLESDFMQFISSNEVYIIEDSFKLNSGKNTLLSKYKIKESVENDIKRAQGIS 137				

```

Db      1387 FLDVLESIDLMQFKHISNVEYIIEDSFKLINSEOKNTLLSKYKIKESVENDIKFAQEGIS 1446
Qy      138 YEEKVLAKYKODLESIKKVIKEEKEKPPSPPTTPEPPAKTDEQKESKFLPLTNIETL 197
Db      1447 YEEKVLAKYKODLESIKKVIKEEKEKPPSPPTTPEPPAKTDEQKESKFLPLTNIETL 1506
Qy      198 YNNLVNKIDYVLINLAKINCNEKDEAHVYKTKLSDLKAIIDKIDLFPKNPYDEFAIKK 257
Db      1507 YNNLVNKIDYVLINLAKINCNEKDEAHVYKTKLSDLKAIIDKIDLFPKNPYDEFAIKK 1566
Qy      358 LINDTKKDMGKGLSTGLVONFPNTIISKLEGFQDMNLISQHCVKQCPENSGCFR 317
Db      1567 LINDTKKDMGKGLSTGLVONFPNTIISKLEGFQDMNLISQHCVKQCPENSGCFR 1626
Qy      318 HLDREBECKCLLNKQEGDKCVENPPTCNENNGCGDADATCTEEDSGSSRKKITCECTK 377
Db      1627 HLDREBECKCLLNKQEGDKCVENPPTCNENNGCGDADATCTEEDSGSSRKKITCECTK 1686
Qy      378 PDSYPLPDGIFCSS 391
Db      1687 PDSYPLPDGIFCSS 1700

```

## RESULT 2

Q810U8.PLA7  
ID Q810U8.PLA7 PRELIMINARY; PRT; 1720 AA.

```

DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Merozoite surface protein 1.
GN Name=PF11475w;
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=36329;

```

## NUCLEOTIDE SEQUENCE.

```

RA MEDLINE=2255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Bertrman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooke K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Corton C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corron C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornaby T., Holroyd S., Horrocks P.,
RA Humphrey S., Jagals K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Kontorov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moutle S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajadream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrett B.G.,
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."
RL Nature 419:527-531 (2002).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
similarity).
CC EMBL; AL929358; CAD51981.1; -; Genomic_DNA.
CC HSSP; P04933; ICEJ.
DR SMR; O810U8; 1607-1699.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR010901; MSP1_C.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07462; MSP1_C; 1.
DR Membrane; Merozoite; Repeat.
SQ SEQUENCE 1720 AA; 195726 MW; 549926C112475DA0 CRC64;

```

Query Match 94.9%; Score 1965; DB 2; Length 1720;  
Best Local Similarity 100.0%; Pred. No. 1.3e-90;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      18 AISTVMDNIISGFENEYDVIYKPLAGYRSLKQIEKNITFTFNLNDIINSRLKGRKY 77
Db      1327 AISTVMDNIISGFENEYDVIYKPLAGYRSLKQIEKNITFTFNLNDIINSRLKGRKY 1386
Qy      78 FLDVLESIDLMQFKHISNVEYIIEDSFKLINSEOKNTLLSKYKIKESVENDIKFAQEGIS 137
Db      1387 FLDVLESIDLMQFKHISNVEYIIEDSFKLINSEOKNTLLSKYKIKESVENDIKFAQEGIS 1446
Qy      138 YEEKVLAKYKODLESIKKVIKEEKEKPPSPPTTPEPPAKTDEQKESKFLPLTNIETL 197
Db      1447 YEEKVLAKYKODLESIKKVIKEEKEKPPSPPTTPEPPAKTDEQKESKFLPLTNIETL 1506
Qy      198 YNNLVNKIDYVLINLAKINCNEKDEAHVYKTKLSDLKAIIDKIDLFPKNPYDEFAIKK 257
Db      1507 YNNLVNKIDYVLINLAKINCNEKDEAHVYKTKLSDLKAIIDKIDLFPKNPYDEFAIKK 1566
Qy      258 LINDTKKDMGKGLSTGLVONFPNTIISKLEGFQDMNLISQHCVKQCPENSGCFR 317
Db      1567 LINDTKKDMGKGLSTGLVONFPNTIISKLEGFQDMNLISQHCVKQCPENSGCFR 1626
Qy      318 HLDREBECKCLLNKQEGDKCVENPPTCNENNGCGDADATCTEEDSGSSRKKITCECTK 377
Db      1627 HLDREBECKCLLNKQEGDKCVENPPTCNENNGCGDADATCTEEDSGSSRKKITCECTK 1686
Qy      378 PDSYPLPDGIFCSS 391
Db      1687 PDSYPLPDGIFCSS 1700

```

## RESULT 3

Q25923.PLA7  
ID Q25923.PLA7 PRELIMINARY; PRT; 652 AA.

```

AC Q25923;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Merozoite surface antigen 1 (Fragment).
GN Name=gp190; Synonym=MSA1, MSP1, PMSA;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=5633;

```

## NUCLEOTIDE SEQUENCE.

```

RA MEDLINE=95354793; PubMed=7628566; DOI=10.1006/expr.1995.1091;
RA Tolle R., Bujard H., Cooper J.A.;
RT "Plasmodium falciparum: variations within the C-terminal region of
merozoite surface antigen-1."
RL Exp. Parasitol. 81:47-54 (1995).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
similarity).
CC EMBL; Z55328; CNA84557.1; -; Genomic_DNA.
CC HSSP; P04933; ICEJ.
DR SMR; Q25923; 539-631.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR010901; MSP1_C.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07462; MSP1_C; 1.
DR Membrane; Merozoite; 1.
FT NON_TER 1
SQ SEQUENCE 652 AA; 74293 MW; 286A87737B490A62 CRC64;

```

Query Match 94.7%; Score 1961; DB 2; Length 652;  
Best Local Similarity 99.7%; Pred. No. 7.3e-91;  
Matches 373; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

Qy      18 AISTVMDNIISGFENEYDVIYKPLAGYRSLKQIEKNITFTFNLNDIINSRLKGRKY 77
Db      259 AISTVMDNIISGFENEYDVIYKPLAGYRSLKQIEKNITFTFNLNDIINSRLKGRKY 318
Qy      78 FLDVLESIDLMQFKHISNVEYIIEDSFKLINSEOKNTLLSKYKIKESVENDIKFAQEGIS 137

```



```

Db 319 FLVLESIDLMQFKHISNEYIIEDSFKLINSEQKNTLLKSYKYIKESYENDIKFAQEGIS 378
QY YEKVLAKYKODLESISKVYIKEKEKPPSPPTTPEPPAKTDEOKKESKFLPLNIETL 197
Db YEKVLAKYKODLESISKVYIKEKEKPPSPPTTPEPPAKTDEOKKESKFLPLNIETL 438
QY YNNLVNKIDYILINKAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLFKNPYDEAIAIK 257
Db YNNLVNKIDYILINKAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLFKNPYDEAIAIK 498
QY LINDTTKMDLGLKISTGLVONFPNTTISKLEGGFQDMLNISQHCYKQCPENSGCGR 317
Db LINDTTKMDLGLKISTGLVONFPNTTISKLEGGFQDMLNISQHCYKQCPENSGCGR 558
QY HLDREBECKCLLNTYQOEGDKCVENPPTCNENNGCCDADATCTEEDSGSSRRKKTCECTK 377
Db HLDREBECKCLLNTYQOEGDKCVENPPTCNENNGCCDADATCTEEDSGSSRRKKTCECTK 618
QY PDSYPLFDGIFCSS 391
Db PDSYPLFDGIFCSS 632

```

## RESULT 4

```

025723 PLAFPA PRELIMINARY; PRT; 373 AA.
ID 025723 PLAFPA PRELIMINARY; PRT; 373 AA.
AC 025723
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mezozoite surface protein 1, 42 kDa C-terminal region (Fragment).
GN Name=MSPI-1;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5633;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Shi Y.-P., Alpern M.P., Poyoa M.M., Nahlen B.L., Oloo A.G., Lal A.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
similarity).
EMBL: U20728; AAA62219.1; -; Genomic_DNA.
DR HSSP; Q25976; IOB1.
DR SMR; Q25723; 281-373.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07462; MSP1_C; 1.
DR Membrane; Mezozoite.
KM Membrane; Mezozoite.
FT NON_TER 1
FT NON_TER 373
SQ SEQUENCE 373 AA; 42849 MW; EE9A891631DE174F CRC64;

```

Query Match 93.8%; Score 1942; DB 2; Length 373;

Best Local Similarity 98.9%; Pred. No. 3.6e-90;

Matches 369; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

QY 18 AISTVMDNITLGFENEYDVITLKLPLAGYRSIAKQIEKNIPTFNINLNDILNSRLKRRY 77
Db AISTVMDNITLGFENEYDVITLKLPLAGYRSIAKQIEKNIPTFNINLNDILNSRLKRRY 60
QY 78 FLVLESIDLMQFKHISNEYIIEDSFKLINSEQKNTLLKSYKYIKESYENDIKFAQEGIS 137
Db FLVLESIDLMQFKHISNEYIIEDSFKLINSEQKNTLLKSYKYIKESYENDIKFAQEGIS 120
QY YEKVLAKYKODLESISKVYIKEKEKPPSPPTTPEPPAKTDEOKKESKFLPLNIETL 197
Db YEKVLAKYKODLESISKVYIKEKEKPPSPPTTPEPPAKTDEOKKESKFLPLNIETL 180
QY YNNLVNKIDYILINKAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLFKNPYDEAIAIK 257

```

```

Db 161 YNNLVNKIDYILINKAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLFKNPYDEAIAIK 240
QY LINDTTKMDLGLKISTGLVONFPNTTISKLEGGFQDMLNISQHCYKQCPENSGCGR 317
Db LINDTTKMDLGLKISTGLVONFPNTTISKLEGGFQDMLNISQHCYKQCPENSGCGR 300
QY HLDREBECKCLLNTYQOEGDKCVENPPTCNENNGCCDADATCTEEDSGSSRRKKTCECTK 377
Db HLDREBECKCLLNTYQOEGDKCVENPPTCNENNGCCDADATCTEEDSGSSRRKKTCECTK 360
QY PDSYPLFDGIFCSS 390
Db PDSYPLFDGIFCSS 373

```

## RESULT 5

```

025723 PLAFPA PRELIMINARY; PRT; 570 AA.
ID 025723 PLAFPA PRELIMINARY; PRT; 570 AA.
AC 025723
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Major mezozoite surface protein (Fragment).
GN Name=MSPI1;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5633;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=88011243; PubMed=3079521;
RA Tanabe K., Mackay M., Goman M., Scalfe J.G.;
RL "Allelic dimorphism in a surface antigen gene of the malaria parasite Plasmodium falciparum."
RT J. Mol. Biol. 195:273-287(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93295445; PubMed=8515786; DOI=10.1016/0166-6851(93)90010-U;
RA Jongwutives S., Tanabe K., Kanbara H.;
RL "Sequence conservation in the C-terminal part of the precursor to the major mezozoite surface proteins (MSPI) of Plasmodium falciparum from field isolates."
RT J. Mol. Biochem. Parasitol. 59:95-100(1993).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
similarity).
EMBL: D13343; BA02604.1; -; Genomic_DNA.
DR HSSP; P04933; ICB1.
DR SMR; Q9TYG2; 457-549.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR010901; MSP1_C.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07462; MSP1_C; 1.
DR Membrane; Mezozoite.
KM Membrane; Mezozoite.
FT NON_TER 1
FT NON_TER 570
SQ SEQUENCE 570 AA; 86740 MW; 8674DEC09B2D662A CRC64;

```

Query Match 93.8%; Score 1942; DB 2; Length 570;

Best Local Similarity 99.2%; Pred. No. 5.7e-90;

Matches 371; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 18 AISTVMDNITLGFENEYDVITLKLPLAGYRSIAKQIEKNIPTFNINLNDILNSRLKRRY 77
Db AISTVMDNITLGFENEYDVITLKLPLAGYRSIAKQIEKNIPTFNINLNDILNSRLKRRY 236
QY 78 FLVLESIDLMQFKHISNEYIIEDSFKLINSEQKNTLLKSYKYIKESYENDIKFAQEGIS 137
Db FLVLESIDLMQFKHISNEYIIEDSFKLINSEQKNTLLKSYKYIKESYENDIKFAQEGIS 296
QY YEKVLAKYKODLESISKVYIKEKEKPPSPPTTPEPPAKTDEOKKESKFLPLNIETL 197
Db YEKVLAKYKODLESISKVYIKEKEKPPSPPTTPEPPAKTDEOKKESKFLPLNIETL 356

```

```
QY 198 YNNLVNKIDYVLINLAKKINCNEKDEAHVYKITKLSDLKAIIDKIDLFKNPYDEAIAK 257
    |||||
Db 357 YNNLVNKIDYVLINLAKKINCNEKDEAHVYKITLSDLKAIIDKIDLFKNPYDEAIAK 416
QY 258 LINDTKKDMGKLLSTGLVONFPNTIISKLEGFQDMLNISQHCYKQCPENSGCFR 317
    |||||
Db 417 LINDTKKDMGKLLSTGLVONFPNTIISKLEGFQDMLNISQHCYKQCPENSGCFR 476
QY 318 HLDREBECKCLNTYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRRKITTCECTK 377
    |||||
Db 477 HLDREBECKCLNTYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRRKITTCECTK 536
QY 378 PDSYPLFDGIFCSS 391
    |||||
Db 537 PDSYPLFDGIFCSS 550

RESULT 6
Q25968 PLAFPA PRELIMINARY; PRT; 570 AA.
ID Q25968
AC Q25968
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Major merozoitte surface protein (fragment).
GN Name=MSPI;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93293445; PubMed=8515786; DOI=10.1016/0166-6851(93)9010-U;
RA Jongmuitwee S., Tanabe K., Kanbara H.;
RT "Sequence conservation in the C-terminal part of the precursor to the
RT major merozoitte surface proteins (MSPI) of Plasmodium falciparum from
RT field isolates."
RL Mol. Biochem. Parasitol. 59:95-100(1993).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
DR EMBL; D13345; BAA02606.1; -, Genomic_DNA.
DR HSSP; P04933; ICBJ.
DR SMK; Q25968; 457-549.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR010901; MSPI_C.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07462; MSPI_C; 1.
DR Membrane; Merozoitte.
FT NON TER
SQ SEQUENCE 570 AA; 46432 MW; 424BF553CCC2F2BE CRC64;

Query Match 93.8%; Score 1942; DB 2; Length 570;
Best Local Similarity 99.2%; Pred. No. 5.7e-90;
Matches 371; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 AISTYMDNIISGFENEYDVILKPLAGYRSLKQIEKNITFPNLNDILNSRLKRRKY 77
    |||||
Db 177 AISTYMDNIISGFENEYDVILKPLAGYRSLKQIEKNITFPNLNDILNSRLKRRKY 236
QY 78 FLVDLESQDMQFKHISNEEYIIEDSFKLNSEQKNTLLKSYKIKESYENDIKFAQEGIS 137
    |||||
Db 237 FLVDLESQDMQFKHISNEEYIIEDSFKLNSEQKNTLLKSYKIKESYENDIKFAQEGIS 296
QY 138 YYEKVLAKYKDDLESIKKVIKEEKEKPPSSPTTPSPAKTDEQKESKFLPFLNIETL 197
    |||||
Db 297 YYEKVLAKYKDDLESIKKVIKEEKEKPPSSPTTPSPAKTDEQKESKFLPFLNIETL 356
QY 198 YNNLVNKIDYVLINLAKKINCNEKDEAHVYKITLSDLKAIIDKIDLFKNPYDEAIAK 257
    |||||
Db 357 YNNLVNKIDYVLINLAKKINCNEKDEAHVYKITLSDLKAIIDKIDLFKNPYDEAIAK 416
QY 258 LINDTKKDMGKLLSTGLVONFPNTIISKLEGFQDMLNISQHCYKQCPENSGCFR 317
    |||||
```

```
Db 417 LINDTKKDMGKLLSTGLVONFPNTIISKLEGFQDMLNISQHCYKQCPENSGCFR 476
QY 318 HLDREBECKCLNTYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRRKITTCECTK 377
    |||||
Db 477 HLDREBECKCLNTYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRRKITTCECTK 536
QY 378 PDSYPLFDGIFCSS 391
    |||||
Db 537 PDSYPLFDGIFCSS 550

RESULT 7
Q764L1 PLAFPA PRELIMINARY; PRT; 1694 AA.
ID Q764L1
AC Q764L1
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Merozoitte surface protein 1.
GN Name=mspi;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tanabe K., Sakihama N., Kaneko A.;
RT "Strable SNPs in Malaria Antigen Genes in Isolated Populations."
RL Science 303:493-493(2004).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
DR EMBL; AB116598; BAB08400.1; -, Genomic_DNA.
DR HSSP; Q25659; 189W.
DR SMK; Q764L1; 1581-1673.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR010901; MSPI_C.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07462; MSPI_C; 1.
DR Membrane; Merozoitte; Repeat.
SQ SEQUENCE 1694 AA; 193467 MW; 661419924EE7F694 CRC64;

Query Match 93.8%; Score 1942; DB 2; Length 1694;
Best Local Similarity 99.2%; Pred. No. 1.9e-89;
Matches 371; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 AISTYMDNIISGFENEYDVILKPLAGYRSLKQIEKNITFPNLNDILNSRLKRRKY 77
    |||||
Db 1301 AISTYMDNIISGFENEYDVILKPLAGYRSLKQIEKNITFPNLNDILNSRLKRRKY 1360
QY 78 FLVDLESQDMQFKHISNEEYIIEDSFKLNSEQKNTLLKSYKIKESYENDIKFAQEGIS 137
    |||||
Db 1361 FLVDLESQDMQFKHISNEEYIIEDSFKLNSEQKNTLLKSYKIKESYENDIKFAQEGIS 1420
QY 138 YYEKVLAKYKDDLESIKKVIKEEKEKPPSSPTTPSPAKTDEQKESKFLPFLNIETL 197
    |||||
Db 1421 YYEKVLAKYKDDLESIKKVIKEEKEKPPSSPTTPSPAKTDEQKESKFLPFLNIETL 1480
QY 198 YNNLVNKIDYVLINLAKKINCNEKDEAHVYKITLSDLKAIIDKIDLFKNPYDEAIAK 257
    |||||
Db 1481 YNNLVNKIDYVLINLAKKINCNEKDEAHVYKITLSDLKAIIDKIDLFKNPYDEAIAK 1540
QY 258 LINDTKKDMGKLLSTGLVONFPNTIISKLEGFQDMLNISQHCYKQCPENSGCFR 317
    |||||
Db 1541 LINDTKKDMGKLLSTGLVONFPNTIISKLEGFQDMLNISQHCYKQCPENSGCFR 1600
QY 318 HLDREBECKCLNTYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRRKITTCECTK 377
    |||||
Db 1601 HLDREBECKCLNTYKQEDKCVENPPTCNENNGCCDADATCTBEDSGSSRRKITTCECTK 1660
QY 378 PDSYPLFDGIFCSS 391
    |||||
```

DB 1661 PD5YPLFDGIFCSS 1674

RESULT 8

MSPL\_PLAFM STANDARD; PRT; 1701 AA.

ID MSPL\_PLAFM

AC P13819;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Merozoite surface protein 1 precursor (Merozoite surface antigens)

DE (PMMSA).

GN Name=MSP-1;

OS Plasmodium falciparum (Isolate FC27 / Papua New Guinea).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI\_TaxID=5837;

[1]

RT NUCLEOTIDE SEQUENCE.

RA MEDLINE=8814299; PubMed=2449612; DOI=10.1016/0166-6851(88)90049-7;

RA Peterson M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G., Brown G.V., Anders R.F., Kemp D.J.;

RT "Variation in the precursor to the major merozoite surface antigens of Plasmodium falciparum.";

RL Mol. Biochem. Parasitol. 27:291-302(1988).

CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -1- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 42 kDa and 19 kDa antigens which are the major surface antigens of merozoites. The maturation take place during schizont.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -----

CC EMBL; M19143; AAA29653.1; -, mRNA.

DR PIR; A54498; A54498.

DR HSSP; P04933; 1CEJ.

DR SMR; P13819; 1588-1680.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR010901; MSPL\_C.

DR Pfam; PF07462; MSPL\_C; 1.

DR Glycoprotein; GPI-anchor; Lipoprotein; Malaria; Membrane; Merozoite; Polypeptide; Repeat; Signal.

KW SIGNAL

FT CHAIN 1 19 Potential.

FT PROPEP 20 1680 Merozoite surface protein 1.

FT LIPID 1681 1701 Removed in mature form (By similarity).

FT LIPID 1680 1680 GPI-anchor amidated serine (By similarity).

FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 239 239 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 470 470 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 607 607 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 802 802 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 899 899 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 919 919 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 965 965 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 991 991 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 1089 1089 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 1196 1196 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 1588 1588 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 1701 AA; 193720 MW; 3920B75E73J38552 CRC64;

Query Match 93.8%; Score 1942; DB 1; Length 1701;

Best Local Similarity 99.2%; Pred. No. 1.9e-89;

Matches 371; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 AISTYMDNIIISGFENEYDVYILKPLAGYRRSLKQIEKNIFFPNLNDILNSRLKKRY 77

DB 1308 AISTYMDNIIISGFENEYDVYILKPLAGYRRSLKQIEKNIFFPNLNDILNSRLKKRY 1367

QY 78 FLDVLESIDLMQFKHISNSNEYIIEDSFKLINSBOKNTLKSXYKIKESVENDIKFAQEGIS 137

DB 1368 FLDVLESIDLMQFKHISNSNEYIIEDSFKLINSBOKNTLKSXYKIKESVENDIKFAQEGIS 1427

QY 138 YYEKYLAKYKODLEISIKYIKKEKEKFPSSPTTTPSPAKTDEOKKESKFLPLNTIEL 197

DB 1428 YYEKYLAKYKODLEISIKYIKKEKEKFPSSPTTTPSPAKTDEOKKESKFLPLNTIEL 1487

QY 198 YNNLVNKIDYILNFKAKINDCNVEKDEAHVYITLSDKAITDKIDIPJNPYDFAIK 257

DB 1488 YNNLVNKIDYILNFKAKINDCNVEKDEAHVYITLSDKAITDKIDIPJNPYDFAIK 1547

QY 258 LINDDTKMDLGLKLTSTGVNFPNTIISKLEKFPDMLNISQHCYKQCPENSGCPR 317

DB 1548 LINDDTKMDLGLKLTSTGVNFPNTIISKLEKFPDMLNISQHCYKQCPENSGCPR 1607

QY 318 HIDERBECKCLINYQEGDKYENPNPTCNENGGCDADATTEBDSGSSRKKTICECTK 377

DB 1608 HIDERBECKCLINYQEGDKYENPNPTCNENGGCDADATTEBDSGSSRKKTICECTK 1667

QY 378 PD5YPLFDGIFCSS 391

DB 1668 PD5YPLFDGIFCSS 1681

RESULT 9

MSPL\_PLAFM STANDARD; PRT; 1701 AA.

ID MSPL\_PLAFM

AC P08569;

DT 01-AUG-1988 (Rel. 08, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Merozoite surface protein 1 precursor (Merozoite surface antigens)

DE (PMMSA) (P190).

GN Name=MSP-1;

OS Plasmodium falciparum (Isolate mad20 / Papua New Guinea).

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI\_TaxID=70153;

RT NUCLEOTIDE SEQUENCE.

RA MEDLINE=88011243; PubMed=3079521;

RA Tanabe K., Mackay M., Goman M., Scaife J.G.;

RT "Allelic dimorphism in a surface antigen gene of the malaria parasite Plasmodium falciparum.";

RL J. Mol. Biol. 195:273-287(1987).

RN [2]

RP SEQUENCE REVISION TO 821; 1220; 1403; 1569 AND 1629.

RA Tanabe K.;

RL Submitted (NOV-2003) to the EMBL/Genbank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE OF 1-115.

RX MEDLINE=86136024; PubMed=3004972;

RA Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U., Stunnenberg H., Bujard H.;

RT "Polymorphism of the precursor for the major surface antigens of Plasmodium falciparum merozoites: studies at the genetic level.";

RL EMBD J. 4:3823-3829(1985).

CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC -1- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 42 kDa and 19 kDa antigens which are the major surface antigens of merozoites. The maturation take place during schizont.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -----

CC EMBL; X05624; CA829112.2; -, Genomic\_DNA.

DR HSSP; P04933; 1CEJ.

DR SMR; P08569; 1588-1680.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR010901; MSPL\_C.

DR Pfam: PF00008; EGF; 1.  
 DR Pfam: PF07462; MSP1\_C; 1.  
 KW Glycoprotein; GPI-anchor; Lipoprotein; Malaria; Membrane; Merozoite;  
 KM Polypeptide; Repeat; Signal.  
 FT SIGNAL 1 19 Potential.  
 FT CHAIN 20 1680 Merozoite surface protein 1.  
 FT PROSEP 1681 1701 Removed in mature form (By similarity).  
 FT LIPID 1680 1680 GPI-anchor amidated serine (By similarity).

Query Match 93.8%; Score 1942; DB 1; Length 1701;  
 Best Local Similarity 99.2%; Pred. No. 1,9e-89;

Matches 371; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 18 AISTMDNLSGFENEVDYIYKPLAGVYRSJKQIEKNIFFPNLNDILNSRLKKRY 77  
 DB 1308 AISTMDNLSGFENEVDYIYKPLAGVYRSJKQIEKNIFFPNLNDILNSRLKKRY 1367  
 OY 78 FLVDLESQDMQFKHISNEEYIIEDSFKLNSQKNTLLSKYIKESYENDIKFAQEGIS 137  
 DB 1368 FLVDLESQDMQFKHISNEEYIIEDSFKLNSQKNTLLSKYIKESYENDIKFAQEGIS 1427  
 OY 138 YYEKVLAKYKDDLESIKKYIKEEKKFPSSPTTPSPAKTDEQKESKFLPLNIETL 197  
 DB 1428 YYEKVLAKYKDDLESIKKYIKEEKKFPSSPTTPSPAKTDEQKESKFLPLNIETL 1487  
 OY 198 YNNLVNKIDYILINKAKINDCNVEKDEAHVKITLSDLKAIIDKIDLFKAPYDEAIKK 257  
 DB 1488 YNNLVNKIDYILINKAKINDCNVEKDEAHVKITLSDLKAIIDKIDLFKAPYDEAIKK 1547  
 OY 258 LINDTKKDMIGKLLSTGLVONFPNTIISKLEGFQDMLNISQHCYKQCPENSGCFR 317  
 DB 1548 LINDTKKDMIGKLLSTGLVONFPNTIISKLEGFQDMLNISQHCYKQCPENSGCFR 1607  
 OY 318 HLDEREBCKCLNLYQEBDKCVENPPTCNENNGCGDADATCTEBDSGSSRKKTCECTK 377  
 DB 1608 HLDEREBCKCLNLYQEBDKCVENPPTCNENNGCGDADATCTEBDSGSSRKKTCECTK 1667  
 OY 378 PDSYPLFDGIFCSS 391  
 DB 1668 PDSYPLFDGIFCSS 1681

## RESULT 10

Q25722\_PLAFA  
 ID Q25722\_PLAFA PRELIMINARY; PRT; 373 AA.

AC Q25722;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Merozoite surface protein 1, 42 kDa C-terminal region (Fragment).  
 GN Name=MSP-1;  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN NUCLEOTIDE SEQUENCE.  
 RP Shi Y.-P., Alpers M.P., Poyva M.M., Nahlen B.L., Oloo A.G., Lal A.A.;  
 RA Submitted (Feb-1995) to the EMBL/GenBank/DBJ databases.

CC -I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).  
 DR EMBL: U20727; AAA62218.1; -; Genomic\_DNA.  
 DR HSSP: Q25976; 1081.  
 DR SMR: Q25722; 281-373.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0009405; P:patogenesis; IEA.  
 DR InterPro: IPR006209; EGF like.  
 DR InterPro: IPR010901; MSP1\_C.  
 DR Pfam: PF00008; EGF; 1.  
 DR Pfam: PF07462; MSP1\_C; 1.  
 KW Membrane; Merozoite.  
 FT NON\_TER 1  
 FT NON\_TER 373  
 SQ SEQUENCE 373 AA; 42871 MW; D29DC2517DDE1B4A CRC64;

Query Match 93.4%; Score 1935; DB 2; Length 373;  
 Best Local Similarity 98.7%; Pred. No. 8.1e-90;

Matches 368; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 18 AISTMDNLSGFENEVDYIYKPLAGVYRSJKQIEKNIFFPNLNDILNSRLKKRY 77  
 DB 1 AISTMDNLSGFENEVDYIYKPLAGVYRSJKQIEKNIFFPNLNDILNSRLKKRY 60  
 OY 78 FLVDLESQDMQFKHISNEEYIIEDSFKLNSQKNTLLSKYIKESYENDIKFAQEGIS 137  
 DB 61 FLVDLESQDMQFKHISNEEYIIEDSFKLNSQKNTLLSKYIKESYENDIKFAQEGIS 120  
 OY 138 YYEKVLAKYKDDLESIKKYIKEEKKFPSSPTTPSPAKTDEQKESKFLPLNIETL 197  
 DB 121 YYEKVLAKYKDDLESIKKYIKEEKKFPSSPTTPSPAKTDEQKESKFLPLNIETL 180  
 OY 198 YNNLVNKIDYILINKAKINDCNVEKDEAHVKITLSDLKAIIDKIDLFKAPYDEAIKK 257  
 DB 191 YNNLVNKIDYILINKAKINDCNVEKDEAHVKITLSDLKAIIDKIDLFKAPYDEAIKK 240  
 OY 258 LINDTKKDMIGKLLSTGLVONFPNTIISKLEGFQDMLNISQHCYKQCPENSGCFR 317  
 DB 241 LINDTKKDMIGKLLSTGLVONFPNTIISKLEGFQDMLNISQHCYKQCPENSGCFR 300  
 OY 318 HLDEREBCKCLNLYQEBDKCVENPPTCNENNGCGDADATCTEBDSGSSRKKTCECTK 377  
 DB 301 HLDEREBCKCLNLYQEBDKCVENPPTCNENNGCGDADATCTEBDSGSSRKKTCECTK 360  
 OY 378 PDSYPLFDGIFCSS 390  
 DB 361 PDSYPLFDGIFCSS 373

## RESULT 11

Q25727\_PLAFA  
 ID Q25727\_PLAFA PRELIMINARY; PRT; 373 AA.

AC Q25727;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Merozoite surface protein 1, 42 kDa C-terminal region (Fragment).  
 GN Name=MSP-1;  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN NUCLEOTIDE SEQUENCE.  
 RP Shi Y.-P., Alpers M.P., Poyva M.M., Nahlen B.L., Oloo A.G., Lal A.A.;  
 RA Submitted (Feb-1995) to the EMBL/GenBank/DBJ databases.  
 CC -I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).  
 DR EMBL: U20732; AAA62223.1; -; Genomic\_DNA.  
 DR HSSP: Q25976; 1081.  
 DR SMR: Q25727; 281-373.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0009405; P:patogenesis; IEA.  
 DR InterPro: IPR006209; EGF like.

DR InterPro; IPR010901; MSP1\_C.  
 DR Pfam; PF00008; EGF\_1.  
 DR Pfam; PF07462; MSP1\_C; 1.  
 KM Membrane; Merozoite.  
 FT NON\_TER 1  
 FT NON\_TER 373  
 SQ SEQUENCE 373 AA; 42815 MW; A79966CF38C405C CRC64;

Query Match 93.3%; Score 1933; DB 2; Length 373;  
 Best Local Similarity 98.9%; Pred. No. 1e-89;  
 Matches 369; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 18 AISTVMDNILSGFENEVDYILKPLAGYRSLLKQIEKNIFTFNINLNDILNSRLKRRY 77  
 DB 1 AISTVMDNILSGFENEVDYILKPLAGYRSLLKQIEKNIFTFNINLNDILNSRLKRRY 60  
 QY 78 FLVDLESDFMQFKHISNNEYIIEDSFKLNSQKNTLLSKYKIKESYENDIKFAQEGIS 137  
 DB 61 FLVDLESDFMQFKHISNNEYIIEDSFKLNSQKNTLLSKYKIKESYENDIKFAQEGIS 120  
 QY 138 YYEKVLAKYKODLESIKKVIKEEKEFPSSPPTTPPSPAKTDEOKKESKFLPLTNITL 197  
 DB 121 YYEKVLAKYKODLESIKKVIKEEKEFPSSPPTTPPSPAKTDEOKKESKFLPLTNITL 180  
 QY 198 YNNLVNKKIDYILNKKAKINDCNVEKDEAHVKITKLSDKAIDDKIDLFPKNPYDEALIK 257  
 DB 181 YNNLVNKKIDYILNKKAKINDCNVEKDEAHVKITKLSDKAIDDKIDLFPKNPYDEALIK 240  
 QY 258 LINDTKKDMGLKLTSLGVNFPNTIISKLEGFQDMLNISQHCYKQCPENSGGFR 317  
 DB 241 LINDTKKDMGLKLTSLGVNFPNTIISKLEGFQDMLNISQHCYKQCPENSGGFR 300  
 QY 318 HLDERECKCLLNTYKQEBDKCVENPPTCNENNGCCDADATCTEBSSSKKKTCECTK 377  
 DB 301 HLDERECKCLLNTYKQEBDKCVENPPTCNENNGCCDADATCTEBSSSKKKTCECTK 360  
 QY 378 PDSYPLFDGIFCS 390  
 DB 361 PDSYPLFDGIFCS 373

RESULT 12  
 ID 025978 PLAFA PRELIMINARY; PRT; 569 AA.  
 AC Q25978\_1 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Major merozoite surface protein (Fragment).  
 GN Name=MSP1;  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93295445; PubMed=8515786; DOI=10.1016/0166-6851(93)90010-U;  
 RA Tongvutwong S., Tanabe K., Kanbara H.;  
 RT "Sequence conservation in the C-terminal part of the precursor to the  
 RT major merozoite surface proteins (MSP1) of Plasmodium falciparum from  
 RT field isolates."  
 RL Mol. Biochem. Parasitol. 59:95-100 (1993).  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By  
 CC similarity).  
 CC EMBL; D1351; BAA02612.1; -, Genomc\_DNA.  
 DR HSSP; P04933; 1CEJ.  
 DR SMR; Q25978; 456-548.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR006309; EGF-like.  
 DR InterPro; IPR010901; MSP1\_C.  
 DR Pfam; PF00008; EGF\_1.  
 DR Pfam; PF07462; MSP1\_C; 1.  
 KM Membrane; Merozoite.

FT NON\_TER 1  
 SQ SEQUENCE 569 AA; 64536 MW; B8B9B63BECB1DA51 CRC64;

Query Match 93.3%; Score 1932.5; DB 2; Length 569;  
 Best Local Similarity 99.2%; Pred. No. 1.7e-89;  
 Matches 371; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 18 AISTVMDNILSGFENEVDYILKPLAGYRSLLKQIEKNIFTFNINLNDILNSRLKRRY 77  
 DB 177 AISTVMDNILSGFENEVDYILKPLAGYRSLLKQIEKNIFTFNINLNDILNSRLKRRY 236  
 QY 78 FLVDLESDFMQFKHISNNEYIIEDSFKLNSQKNTLLSKYKIKESYENDIKFAQEGIS 137  
 DB 237 FLVDLESDFMQFKHISNNEYIIEDSFKLNSQKNTLLSKYKIKESYENDIKFAQEGIS 296  
 QY 138 YYEKVLAKYKODLESIKKVIKEEKEFPSSPPTTPPSPAKTDEOKKESKFLPLTNITL 197  
 DB 297 YYEKVLAKYKODLESIKKVIKEEKEFPSSPPTTPPSPAKTDEOKKESKFLPLTNITL 355  
 QY 198 YNNLVNKKIDYILNKKAKINDCNVEKDEAHVKITKLSDKAIDDKIDLFPKNPYDEALIK 257  
 DB 356 YNNLVNKKIDYILNKKAKINDCNVEKDEAHVKITKLSDKAIDDKIDLFPKNPYDEALIK 415  
 QY 258 LINDTKKDMGLKLTSLGVNFPNTIISKLEGFQDMLNISQHCYKQCPENSGGFR 317  
 DB 416 LINDTKKDMGLKLTSLGVNFPNTIISKLEGFQDMLNISQHCYKQCPENSGGFR 475  
 QY 318 HLDERECKCLLNTYKQEBDKCVENPPTCNENNGCCDADATCTEBSSSKKKTCECTK 377  
 DB 476 HLDERECKCLLNTYKQEBDKCVENPPTCNENNGCCDADATCTEBSSSKKKTCECTK 535  
 QY 378 PDSYPLFDGIFCS 391  
 DB 536 PDSYPLFDGIFCS 549

RESULT 13  
 ID MSP1\_PLAFC STANDARD; PRT; 1726 AA.  
 AC P04934;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Merozoite surface protein 1 precursor (Merozoite surface antigens)  
 DE (PfamSA) (P195).  
 GN Name=MSP-1;  
 OS Plasmodium falciparum (isolate Camp / Malaysia).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5835;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE OF 1-1103.  
 RX MEDLINE=86205236; PubMed=3517809;  
 RA Weber J.L., Leininger W.M., Lyon J.A.;  
 RT "Variation in the gene encoding a major merozoite surface antigen of  
 RT the human malaria parasite Plasmodium falciparum."  
 RL Nucleic Acids Res. 14:3311-3323 (1986).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE OF 1104-1726.  
 RX MEDLINE=88143999; PubMed=3278296;  
 RA Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;  
 RT "Merozoite surface protein sequence from the Camp strain of the human  
 RT malaria parasite Plasmodium falciparum."  
 RL Nucleic Acids Res. 16:1206-1206 (1988).  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -1- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 42  
 CC kDa and 19 kDa antigens which are the major surface antigens of  
 CC merozoites. The maturation take place during schizont.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

```

CC -----
DR EMBL; X03831; CAA27446.1; -; Genomic_DNA.
DR PIR; A23386; SAZQM.
DR HSSP; P04933/1CEJ.
DR SMR; P04934/1613-1705.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR010901; MSP1_C.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07462; MSP1_C_1.
DR Glycoprotein; GPI-anchor; Lipoprotein; Malaria; Membrane; Merozoite;
  Polyprotein; Repeat; Signal.
KM SIGNAL
FT CHAIN 1 19 Potential.
FT PROPEP 20 1705 Merozoite surface protein 1.
FT LIPID 1705 1705 Removed in mature form (By similarity).
  GPI-anchor amidated serine (By
  similarity).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 272 272 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 501 501 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 567 567 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 638 638 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 827 827 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 924 924 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 944 944 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 990 990 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1016 1016 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1114 1114 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1221 1221 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1613 1613 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1726 AA; 196198 MW; DD8AD45FA352BCF3 CRC64;

```

```

Query Match 93.2%; Score 1931; DB 1; Length 1726;
Best Local Similarity 98.7%; Pred. No. 6,8e-89;
Matches 369; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

```

OY 18 AISTVMDNIIISGFENEYDVYILKPLAGVYRSLLKKQIEKNIFFTNLNDILNSRLKKRY 77
DB 1333 AISTVMDNIIISGFENEYDVYILKPLAGVYRSLLKKQIEKNIFFTNLNDILNSRLKKRY 1392
OY 78 FLDVLESIDLMQPKHISSENYIIEDSFKLNSQKNTLLKSYKIKESVENDIKFAQEGIS 137
DB 1333 FLDVLESIDLMQPKHISSENYIIEDSFKLNSQKNTLLKSYKIKESVENDIKFAQEGIS 1452
OY 138 YEKVLAKYKDDLESIKVYKEKEKFPSSPTTPSPAKTDEQKESKLPFLTNIELT 197
DB 1453 YEKVLAKYKDDLESIKVYKEKEKFPSSPTTPSPAKTDEQKESKLPFLTNIELT 1512
OY 198 YNNLVNKIDVYILINKAKINDCNVEKDEAHVYKITLSDLKAIIDKIDLPKQPYDEAIKK 257
DB 1513 YNNLVNKIDVYILINKAKINDCNVEKDEAHVYKITLSDLKAIIDKIDLPKQPYDEAIKK 1572
OY 258 LINDOTKDMIGKLLSTGLGVONFPNTIISKLEGGFODMLNISQCVKQCPENSGGFR 317
DB 1573 LINDOTKDMIGKLLSTGLGVONFPNTIISKLEGGFODMLNISQCVKQCPENSGGFR 1632
OY 318 HLDREBECKCLLNYKQEGDKCVENPPTCNENNGCCDADATCTEEDSSSSRRKITCECTK 377
DB 1633 HLDREBECKCLLNYKQEGDKCVENPPTCNENNGCCDADATCTEEDSSSSRRKITCECTK 1692
OY 378 PDSYPLFDGIFCSS 391
DB 1693 PDSYPLFDGIFCSS 1706

```

```

RESULT 14
MSPI_PLAF3 STANDARD; PRT; 1682 AA.
AC P19598; Q25921;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Merozoite surface protein 1 precursor (Merozoite surface antigens)
DE (P190).

```

```

GN Name=MSP-1;
OS Plasmodium falciparum (isolate ro-33 / Ghana).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5834;
RN [1]
RP NUCLEOTIDE SEQUENCE OF 1-1061.
RX MEDLINE=8816657; Pubmed=3327688;
RA Cerna U., Rotmann D., Matile H., Reber-Liske R.;
RT "A naturally occurring gene encoding the major surface antigen
  precursor p190 of Plasmodium falciparum lacks tripeptide repeats.";
RL EMBL J. 6:4137-4142(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 1032-1682.
RX MEDLINE=95354793; Pubmed=7628566; DOI=10.1006/expr.1995.1091;
RA Tolle R., Bujard H., Cooper J.A.;
RT "Plasmodium falciparum: variations within the C-terminal region of
  merozoite surface antigen-1";
RL Exp. Parasitol. 81:47-54(1995).
CC -1 SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
  Kda and 19 kDa antigens which are the major surface antigens of
  merozoites. The maturation take place during schizont.

```

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

```

DR EMBL; M35727; AAA29715.1; -; mRNA.
DR EMBL; Y00087; CAA68280.1; -; Genomic_DNA.
DR EMBL; Z35326; CAA84555.1; -; Genomic_DNA.
DR HSSP; P04933/1CEJ.
DR SMR; P19598; 1569-1661.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR010901; MSP1_C.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07462; MSP1_C_1.
KM Glycoprotein; GPI-anchor; Lipoprotein; Malaria; Membrane; Merozoite;
  Polyprotein; Repeat; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1661 Merozoite surface protein 1.
FT PROPEP 1662 1682 Removed in mature form (By similarity).
FT LIPID 1661 1661 GPI-anchor amidated serine (By
  similarity).
FT CARBOHYD 233 233 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 462 462 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 528 528 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 599 599 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 785 785 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 881 881 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 901 901 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 947 947 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1071 1071 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1178 1178 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1569 1569 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1682 AA; 192463 MW; C82A1E159948CAD6 CRC64;

```

```

Query Match 93.2%; Score 1930.5; DB 1; Length 1682;
Best Local Similarity 98.7%; Pred. No. 7.1e-89;
Matches 369; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

```

```

OY 18 AISTVMDNIIISGFENEYDVYILKPLAGVYRSLLKKQIEKNIFFTNLNDILNSRLKKRY 77
DB 1290 AISTVMDNIIISGFENEYDVYILKPLAGVYRSLLKKQIEKNIFFTNLNDILNSRLKKRY 1349
OY 78 FLDVLESIDLMQPKHISSENYIIEDSFKLNSQKNTLLKSYKIKESVENDIKFAQEGIS 137
DB 1350 FLDVLESIDLMQPKHISSENYIIEDSFKLNSQKNTLLKSYKIKESVENDIKFAQEGIS 1409
OY 138 YEKVLAKYKDDLESIKVYKEKEKFPSSPTTPSPAKTDEQKESKLPFLTNIELT 197
DB 1410 YEKVLAKYKDDLESIKVYKEKEKFPSSPTTPSPAKTDEQKESKLPFLTNIELT 1468

```

QY 198 YNNLVNKIDYVLINLAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNPFDEFAIKK 257  
DB 1469 YNNLVNKIDYVLINLAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNPFDEFAIKK 1528  
QY 258 LINDTKKMDLGLSTGLVONFPNTTISKLEGGFODMLNISQHCYKQCPENSGGCFR 317  
DB 1529 LINDTKKMDLGLSTGLVONFPNTTISKLEGGFODMLNISQHCYKQCPENSGGCFR 1588  
QY 318 HLDERECKCLLNYKQEGDKCVENPNPTCNENNGCCDADATCTEEDSGSSRRKKTCECTK 377  
DB 1569 HLDERECKCLLNYKQEGDKCVENPNPTCNENNGCCDADATCTEEDSGSSRRKKTCECTK 1648  
QY 378 PDSYPLFDGIFCS 391  
DB 1649 PDSYPLFDGIFCS 1662

## RESULT 15

Q43996 PLAF PA  
ID Q43996 PLAF PRELIMINARY; PRT: 373 AA.  
AC Q43996;  
DT 01-JUN-1998 (TRENBLrel. 06, Created)  
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Merozoite surface protein-1 (Fragment).  
GN Name=MSP-1; falciparum.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Kenya-2;  
RX MEDLINE=98319411; PubMed=9657329; DOI=10.1016/S0166-6851(98)00010-3;  
RA Qari S.H., Shi Y.P., Goldman I.F., Nahlen B.L., Tibayrenc M.,  
Lal A.A.;  
RT "Predicted and observed alleles of Plasmodium falciparum merozoite  
surface protein-1 (MSP-1), a potential malaria vaccine antigen.";  
RL Mol. Biochem. Parasitol. 92:241-252(1998).  
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By  
similarity).  
CC EMBL; AF040568; AAC39098.1; -; Genomic DNA.  
DR HSSP; Q25976; 10B1.  
DR SMR; Q43996; 281-373.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0009405; F:pachyenesist; IEA.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR010901; MSP1\_C.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF07462; MSP1\_C; 1.  
KM Membrane; Merozoite.  
FT NON\_TER 1  
FT TER 373  
SQ SEQUENCE 373 AA; 42903 MW; 86CD4B721E605A5F CRC64;

Query Match 93.1%; Score 1929; DB 2; Length 373;

Best Local Similarity 98.9%; Pred. No. 1.6e-89;  
Matches 369; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 18 AISVTMDNIIISGFENEVDVYILKPLAGVRSLSKQIEKNIFFTNLNDILNSRLKKRY 77  
DB 1 AISVTMDNIIISGFENEVDVYILKPLAGVRSLSKQIEKNIFFTNLNDILNSRLKKRY 60  
QY 78 FLVDIESDLMOFKHISNVEYIIEDSFKLINSQKNTLLKSYKIKESVENDIKFPAQEGIS 137  
DB 61 FLVDIESDLMOFKHISNVEYIIEDSFKLINSQKNTLLKSYKIKESVENDIKFPAQEGIS 120  
QY 138 YYEKYLAKYKODLESIKKVIKKEKPPSPPTTSPSPAKTDEOKKESKFLPFLTNIEFL 197  
DB 121 YYEKYLAKYKODLESIKKVIKKEKPPSPPTTSPSPAKTDEOKKESKFLPFLTNIEFL 180  
QY 198 YNNLVNKIDYVLINLAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNPFDEFAIKK 257

DB 181 YNNLVNKIDYVLINLAKINDCNVEKDEAHVKITKLSDLKAIDDKIDLFKNPFDEFAIKK 240  
QY 258 LINDTKKMDLGLSTGLVONFPNTTISKLEGGFODMLNISQHCYKQCPENSGGCFR 317  
DB 241 LINDTKKMDLGLSTGLVONFPNTTISKLEGGFODMLNISQHCYKQCPENSGGCFR 300  
QY 318 HLDERECKCLLNYKQEGDKCVENPNPTCNENNGCCDADATCTEEDSGSSRRKKTCECTK 377  
DB 301 HLDERECKCLLNYKQEGDKCVENPNPTCNENNGCCDADATCTEEDSGSSRRKKTCECTK 360  
QY 378 PDSYPLFDGIFCS 390  
DB 361 PDSYPLFDGIFCS 373

Search completed: May 5, 2006, 00:24:32  
Job time : 233 secs



**THIS PAGE IS BLANK**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: May 5, 2006, 00:25:32 ; Search time 168 Seconds  
(without alignments)  
972.448 Million cell updates/sec

Title: US-10-057-532A-7  
2071  
Perfect score: 1 MAHHHHHPGSGSGTMAIS.....TCCTKPDSPFLFDICFSS 391  
Sequence:

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2071	100.0	391	4	US-10-057-531A-7 Sequence 7, Appli
2	2071	100.0	391	4	US-10-057-531A-7 Sequence 7, Appli
3	2055	99.2	393	4	US-10-057-531A-3 Sequence 3, Appli
4	2055	99.2	393	4	US-10-057-531A-3 Sequence 3, Appli
5	2008.5	97.0	431	4	US-10-057-531A-2 Sequence 2, Appli
6	2008.5	97.0	431	4	US-10-057-531A-2 Sequence 2, Appli
7	2008.5	97.0	546	4	US-10-057-531A-1 Sequence 1, Appli
8	2008.5	97.0	546	4	US-10-057-531A-1 Sequence 1, Appli
9	1968	95.0	383	4	US-10-057-531A-5 Sequence 5, Appli
10	1968	95.0	383	4	US-10-057-531A-5 Sequence 5, Appli
11	1965	94.9	394	3	US-09-978-756-3 Sequence 3, Appli
12	1931	93.2	394	4	US-10-062-809-2 Sequence 2, Appli
13	1931	93.2	394	4	US-10-062-809-2 Sequence 2, Appli
14	1931	93.2	394	5	US-10-925-385-2 Sequence 5, Appli
15	1931	93.2	394	5	US-10-925-385-2 Sequence 5, Appli
16	1928	93.1	396	5	US-10-062-809-18 Sequence 18, Appli
17	1928	93.1	402	4	US-10-098-514-14 Sequence 14, Appli
18	1928	93.1	402	4	US-10-062-809-16 Sequence 16, Appli
19	1928	93.1	402	5	US-10-935-793-16 Sequence 16, Appli
20	1928	93.1	402	5	US-10-925-385-16 Sequence 16, Appli
21	1921	92.8	394	4	US-10-062-809-3 Sequence 3, Appli
22	1921	92.8	394	5	US-10-935-793-3 Sequence 3, Appli
23	1921	92.8	394	5	US-10-925-385-3 Sequence 3, Appli
24	1911	92.3	383	4	US-10-098-514-4 Sequence 4, Appli
25	1900	91.7	383	4	US-10-098-514-2 Sequence 2, Appli
26	1254.5	60.6	371	4	US-10-404-667-2 Sequence 2, Appli
27	1250.5	60.4	371	4	US-10-404-667-5 Sequence 5, Appli

28	1166.5	56.3	1602	5	US-10-954-924-7 Sequence 7, Appli
29	1166.5	56.3	1621	5	US-10-954-924-5 Sequence 5, Appli
30	1166.5	56.3	1639	4	US-10-087-464-10 Sequence 10, Appli
31	1166.5	56.3	1639	5	US-10-954-924-3 Sequence 3, Appli
32	1166.5	56.3	376	3	US-09-978-756-2 Sequence 2, Appli
33	1165.5	56.3	376	4	US-10-087-464-34 Sequence 34, Appli
34	1165.5	56.3	378	4	US-10-087-464-11 Sequence 11, Appli
35	1163.5	56.2	384	4	US-10-062-809-8 Sequence 8, Appli
36	1163.5	56.2	384	5	US-10-935-793-8 Sequence 8, Appli
37	1163.5	56.2	384	5	US-10-925-385-8 Sequence 8, Appli
38	1161.5	56.1	355	4	US-10-677-641-8 Sequence 8, Appli
39	1161.5	56.1	355	5	US-10-949-975-9 Sequence 9, Appli
40	1161.5	56.1	355	6	US-11-140-676-9 Sequence 9, Appli
41	1161.5	56.1	361	5	US-10-949-975-10 Sequence 10, Appli
42	1161.5	56.1	361	6	US-11-140-676-10 Sequence 10, Appli
43	1154.5	55.7	379	5	US-10-949-975-11 Sequence 11, Appli
44	1154.5	55.7	379	6	US-11-140-676-11 Sequence 11, Appli
45	1040	50.2	377	4	US-10-062-809-5 Sequence 5, Appli

## ALIGNMENTS

RESULT 1  
US-10-057-531A-7  
Sequence 7, Application US/10057531A  
Publication No. US20030161838A1  
GENERAL INFORMATION:  
APPLICANT: Lyon, Jeffrey A.  
TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite  
FILE REFERENCE: 003/241/SAP  
CURRENT APPLICATION NUMBER: US/10/057,531A  
CURRENT FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: US 60/264,535  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: US 60/347,564  
PRIOR FILING DATE: 2001-10-26  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Apple Macintosh Microsoft Word 6.0  
SEQ ID NO 7  
LENGTH: 391  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: E. coli expressed P. falciparum MSP-142 (3D7)  
US-10-057-531A-7

Query Match 100.0%; Score 2071; DB 4; Length 391;  
Best Local Similarity 100.0%; Pred. No. 2.1e-126;  
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAHHHHHPGSGSGTMAISVTMDNISGFENEVDYILKPLAGYRRLKQIENITTF 60
DB	1	MAHHHHHPGSGSGTMAISVTMDNISGFENEVDYILKPLAGYRRLKQIENITTF 60
QY	61	NLNINDIINSRLKRRKFLDVLESDFKHSSEYIIEISFKLNSBOKNTLKSXY 120
DB	61	NLNINDIINSRLKRRKFLDVLESDFKHSSEYIIEISFKLNSBOKNTLKSXY 120
QY	121	IKESVENDIKFAOEGISYKVLAKYKDDLESIKKVIKEEKKEPSSPTTPPSAKTDE 180
DB	121	IKESVENDIKFAOEGISYKVLAKYKDDLESIKKVIKEEKKEPSSPTTPPSAKTDE 180
QY	181	OKESKEFLPFLTNITETLYNNLVNKIDYILNKLAKINDCNVEKDAHYKITLSLKAID 240
DB	181	OKESKEFLPFLTNITETLYNNLVNKIDYILNKLAKINDCNVEKDAHYKITLSLKAID 240
QY	241	DKIDLFKPYDFEAIKKLINDTKDMGLSTGLVONPNTIISKLEGFQDMNIS 300
DB	241	DKIDLFKPYDFEAIKKLINDTKDMGLSTGLVONPNTIISKLEGFQDMNIS 300

```

QY 301 OHQCVKQCPENSGCFRHLDEREBCCKLNTYKQEGDKCVENPPTCNENNGCCDADATCT 360
DB 301 OHQCVKQCPENSGCFRHLDEREBCCKLNTYKQEGDKCVENPPTCNENNGCCDADATCT 360
QY 361 EEDSGSSRRKKTTCCTKPDSPYPLFDGIFCSS 391
DB 361 EEDSGSSRRKKTTCCTKPDSPYPLFDGIFCSS 391

```

## RESULT 2

```

US-10-057-532A-7
; Sequence 7, Application US/10057532A
; Publication No. US20030161839A1
; GENERAL INFORMATION:
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Angov, Evelina
; APPLICANT: Cohen, Joe D.
; APPLICANT: Voss, Gerald
; TITLE OF INVENTION: Recombinant P. falciparum Merozoite Protein-142 Vaccine
; FILE REFERENCE: 003/238/SAP
; CURRENT APPLICATION NUMBER: US/10/057,532A
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/264,535
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/347,564
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 7
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: E. coli expressed P. falciparum MSP-142 (3D7)
US-10-057-532A-7

```

```

Query Match 100.0%; Score 2071; DB 4; Length 391;
Best Local Similarity 100.0%; Pred. No. 2,1e-126;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MAHHHHHPPGSGSGTMAISVTMDNISGFENEYDVIYKPLAGYRSIKKQIEKNITFE 60
DB 1 MAHHHHHPPGSGSGTMAISVTMDNISGFENEYDVIYKPLAGYRSIKKQIEKNITFE 60
QY 61 NLNLDILNSRLKRRKYFLDVLESPLMOFKHISNEYIIEDSFKLNSQKNTLKSXY 120
DB 61 NLNLDILNSRLKRRKYFLDVLESPLMOFKHISNEYIIEDSFKLNSQKNTLKSXY 120
QY 121 IKESVENDIKFAOEGISYIEKVLAKYKDLSESIKVIEKEKEKFPSSPTTPPSPAKTDE 180
DB 121 IKESVENDIKFAOEGISYIEKVLAKYKDLSESIKVIEKEKEKFPSSPTTPPSPAKTDE 180
QY 121 IKESVENDIKFAOEGISYIEKVLAKYKDLSESIKVIEKEKEKFPSSPTTPPSPAKTDE 180
DB 121 IKESVENDIKFAOEGISYIEKVLAKYKDLSESIKVIEKEKEKFPSSPTTPPSPAKTDE 180
QY 181 OKKESKFLPFLNITETLNNLVNKKIDYILNKAKINDCNVEKDEAHVKITLSDLKAD 240
DB 181 OKKESKFLPFLNITETLNNLVNKKIDYILNKAKINDCNVEKDEAHVKITLSDLKAD 240
QY 241 DKIDLFKNPYDEPAIKKLINDTKKMDLSTGLVONFPPTIISKLEGGFQDMLNS 300
DB 241 DKIDLFKNPYDEPAIKKLINDTKKMDLSTGLVONFPPTIISKLEGGFQDMLNS 300
QY 301 OHQCVKQCPENSGCFRHLDEREBCCKLNTYKQEGDKCVENPPTCNENNGCCDADATCT 360
DB 301 OHQCVKQCPENSGCFRHLDEREBCCKLNTYKQEGDKCVENPPTCNENNGCCDADATCT 360
QY 361 EEDSGSSRRKKTTCCTKPDSPYPLFDGIFCSS 391
DB 361 EEDSGSSRRKKTTCCTKPDSPYPLFDGIFCSS 391

```

```

RESULT 3
US-10-057-531A-3
; Sequence 3, Application US/10057531A
; Publication No. US20030161838A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Angov, Evelina
; TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite
; FILE REFERENCE: Protein-142 Vaccine
; CURRENT APPLICATION NUMBER: US/10/057,531A
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/264,535
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/347,564
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 3
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein
US-10-057-531A-3

```

```

Query Match 99.2%; Score 2055; DB 4; Length 393;
Best Local Similarity 99.2%; Pred. No. 2.3e-125;
Matches 390; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

```

```

QY 1 MAHHHHHPPGSGSGTMAISVTMDNISGFENEYDVIYKPLAGYRSIKKQIEKNITFE 58
DB 1 MAHHHHHPPGSGSGTMAISVTMDNISGFENEYDVIYKPLAGYRSIKKQIEKNITFE 60
QY 59 TPNLNDILNSRLKRRKYFLDVLESPLMOFKHISNEYIIEDSFKLNSQKNTLKSXY 118
DB 59 TPNLNDILNSRLKRRKYFLDVLESPLMOFKHISNEYIIEDSFKLNSQKNTLKSXY 120
QY 119 KYIESVENDIKFAOEGISYIEKVLAKYKDLSESIKVIEKEKEKFPSSPTTPPSPAKT 178
DB 119 KYIESVENDIKFAOEGISYIEKVLAKYKDLSESIKVIEKEKEKFPSSPTTPPSPAKT 180
QY 121 KYIESVENDIKFAOEGISYIEKVLAKYKDLSESIKVIEKEKEKFPSSPTTPPSPAKT 180
DB 121 KYIESVENDIKFAOEGISYIEKVLAKYKDLSESIKVIEKEKEKFPSSPTTPPSPAKT 180
QY 179 DEOKESKFLPFLNITETLNNLVNKKIDYILNKAKINDCNVEKDEAHVKITLSDLKAD 238
DB 179 DEOKESKFLPFLNITETLNNLVNKKIDYILNKAKINDCNVEKDEAHVKITLSDLKAD 240
QY 239 IDDKIDLFKNPYDEPAIKKLINDTKKMDLSTGLVONFPPTIISKLEGGFQDMLNS 298
DB 239 IDDKIDLFKNPYDEPAIKKLINDTKKMDLSTGLVONFPPTIISKLEGGFQDMLNS 300
QY 299 ISOHQCVKQCPENSGCFRHLDEREBCCKLNTYKQEGDKCVENPPTCNENNGCCDADAT 358
DB 299 ISOHQCVKQCPENSGCFRHLDEREBCCKLNTYKQEGDKCVENPPTCNENNGCCDADAT 360
QY 359 CTEEDSGSSRRKKTTCCTKPDSPYPLFDGIFCSS 391
DB 359 CTEEDSGSSRRKKTTCCTKPDSPYPLFDGIFCSS 393

```

```

RESULT 4
US-10-057-532A-3
; Sequence 3, Application US/10057532A
; Publication No. US20030161839A1
; GENERAL INFORMATION:
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Angov, Evelina
; APPLICANT: Cohen, Joe D.
; APPLICANT: Voss, Gerald
; TITLE OF INVENTION: Recombinant P. falciparum Merozoite Protein-142 Vaccine
; FILE REFERENCE: 003/238/SAP
; CURRENT APPLICATION NUMBER: US/10/057,532A
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/264,535
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/347,564
; PRIOR FILING DATE: 2001-10-26

```

NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: Apple Macintosh Microsoft Word 6.0  
 SEQ ID NO 3  
 LENGTH: 393  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE:  
 OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein Sequence in  
 US-10-057-532A-3

Query Match 99.2%; Score 2055; DB 4; Length 393;  
 Best Local Similarity 99.2%; Pred. No. 2.3e-125;  
 Matches 390; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 MAHHHHHPGSG--SGGTMAISVTMDNITLSGFENEVDYIYKPLAGVRSLSKKQIEKNIF 58  
 |||||  
 DB 1 MAHHHHHPGSGIEGRGTMAISVTMDNITLSGFENEVDYIYKPLAGVRSLSKKQIEKNIF 60  
 QY 59 TPNLNLNDILNSRLKRRKYFLDVLDESDFMQFHHISSNEYIIEDSFKLINSBOKNTLKSX 118  
 |||||  
 DB 61 TPNLNLNDILNSRLKRRKYFLDVLDESDFMQFHHISSNEYIIEDSFKLINSBOKNTLKSX 120  
 QY 119 KYIKESVENDIKFAOEGISYEKVLAKYKDLESIKKVIKEEKEKFPSSPPTPPSPAKT 178  
 |||||  
 DB 121 KYIKESVENDIKFAOEGISYEKVLAKYKDLESIKKVIKEEKEKFPSSPPTPPSPAKT 180  
 QY 179 DEOKKESFELPLNIEFTLYNNLVNKKIDYILNKAINDCNVEKDEAHVKITKLSDLKA 238  
 |||||  
 DB 181 DEOKKESFELPLNIEFTLYNNLVNKKIDYILNKAINDCNVEKDEAHVKITKLSDLKA 240  
 QY 239 IDDKIDLFPKNPYDFEAIKKLINDPTKDKMLGKLSTGLVQNPNTIISKLEIGKFQDMLN 298  
 |||||  
 DB 241 IDDKIDLFPKNPYDFEAIKKLINDPTKDKMLGKLSTGLVQNPNTIISKLEIGKFQDMLN 300  
 QY 299 ISQHOCVKKQCPENSGCFRHLDERECKCLLNYKQEGKCVENPPTCNENNGCDADAT 358  
 |||||  
 DB 301 ISQHOCVKKQCPENSGCFRHLDERECKCLLNYKQEGKCVENPPTCNENNGCDADAT 360  
 QY 359 CTEEDSGSSRRKKTCTECPKPSYPLFDGIFCSS 391  
 |||||  
 DB 361 CTEEDSGSSRRKKTCTECPKPSYPLFDGIFCSS 393

## RESULT 5

US-10-057-531A-2  
 ; Sequence 2, Application US/10057531A  
 ; Publication No. US20030161838A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lyon, Jeffrey A.  
 ; APPLICANT: Angov, Evelina  
 ; TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite  
 ; TITLE OF INVENTION: Protein-142 Vaccine  
 ; FILE REFERENCE: 003/241/SAP  
 ; CURRENT APPLICATION NUMBER: US/10/057,531A  
 ; PRIOR FILING DATE: 2002-01-25  
 ; PRIOR APPLICATION NUMBER: US 60/264,535  
 ; PRIOR FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: US 60/347,564  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
 ; SEQ ID NO 2  
 ; LENGTH: 431  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein  
 ; OTHER INFORMATION: Sequence in PRT(50)MSP1-42  
 US-10-057-531A-2

Query Match 97.0%; Score 2008.5; DB 4; Length 431;  
 Best Local Similarity 89.5%; Pred. No. 2.7e-122;  
 Matches 385; Conservative 0; Mismatches 4; Indels 41; Gaps 1;

QY 3 HHHHHHPGSG-----SGGTMAISV 21  
 |||||  
 DB 2 HHHHHHSGLVPRSGMKETAARKERQHMDSPDGTDDDDKAMADIGSISGRGTMAISV 61  
 QY 22 TMDNITLSGFENEVDYIYKPLAGVRSLSKKQIEKNIFPNLNLNDILNSRLKRRKYFLDV 81  
 |||||  
 DB 62 TMDNITLSGFENEVDYIYKPLAGVRSLSKKQIEKNIFPNLNLNDILNSRLKRRKYFLDV 121  
 QY 82 LESDMQFHHISSNEYIIEDSFKLINSBOKNTLKSXYIKESVENDIKFAOEGISYEK 141  
 |||||  
 DB 122 LESDMQFHHISSNEYIIEDSFKLINSBOKNTLKSXYIKESVENDIKFAOEGISYEK 181  
 QY 142 VLAKYKDLESIKKVIKEEKEKFPSSPPTPPSPAKTDEOKKESFELPLNIEFTLYNNL 201  
 |||||  
 DB 182 VLAKYKDLESIKKVIKEEKEKFPSSPPTPPSPAKTDEOKKESFELPLNIEFTLYNNL 241  
 QY 202 VNKKIDYILNKAINDCNVEKDEAHVKITKLSDLKAIDDKIDLFPKNPYDFEAIKKLIND 261  
 |||||  
 DB 242 VNKKIDYILNKAINDCNVEKDEAHVKITKLSDLKAIDDKIDLFPKNPYDFEAIKKLIND 301  
 QY 262 DTKDKMLGKLSTGLVQNPNTIISKLEIGKFQDMLNISOHCVKKQCPENSGCFRHLDE 321  
 |||||  
 DB 302 DTKDKMLGKLSTGLVQNPNTIISKLEIGKFQDMLNISOHCVKKQCPENSGCFRHLDE 361  
 QY 322 REECKCLLNYKQEGKCVENPPTCNENNGCDADATCTEEDSGSSRRKKTCTECPKPSY 381  
 |||||  
 DB 362 REECKCLLNYKQEGKCVENPPTCNENNGCDADATCTEEDSGSSRRKKTCTECPKPSY 421  
 QY 382 PLFDGIFCSS 391  
 |||||  
 DB 422 PLFDGIFCSS 431

## RESULT 6

US-10-057-532A-2  
 ; Sequence 2, Application US/10057532A  
 ; Publication No. US20030161839A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lyon, Jeffrey A.  
 ; APPLICANT: Angov, Evelina  
 ; APPLICANT: Cohen, Joe D.  
 ; APPLICANT: Voss, Gerald  
 ; TITLE OF INVENTION: Recombinant P. falciparum Merozoite Protein-142 Vaccine  
 ; FILE REFERENCE: 003/238/SAP  
 ; CURRENT APPLICATION NUMBER: US/10/057,532A  
 ; CURRENT FILING DATE: 2001-01-25  
 ; PRIOR APPLICATION NUMBER: US 60/264,535  
 ; PRIOR FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: US 60/347,564  
 ; PRIOR FILING DATE: 2001-10-26  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
 ; SEQ ID NO 2  
 ; LENGTH: 431  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein Sequence in  
 ; OTHER INFORMATION: PRT(50)MSP1-42  
 US-10-057-532A-2

Query Match 97.0%; Score 2008.5; DB 4; Length 431;  
 Best Local Similarity 89.5%; Pred. No. 2.7e-122;  
 Matches 385; Conservative 0; Mismatches 4; Indels 41; Gaps 1;

QY 3 HHHHHHPGSG-----SGGTMAISV 21  
 |||||  
 DB 2 HHHHHHSGLVPRSGMKETAARKERQHMDSPDGTDDDDKAMADIGSISGRGTMAISV 61  
 QY 22 TMDNITLSGFENEVDYIYKPLAGVRSLSKKQIEKNIFPNLNLNDILNSRLKRRKYFLDV 81  
 |||||  
 DB 62 TMDNITLSGFENEVDYIYKPLAGVRSLSKKQIEKNIFPNLNLNDILNSRLKRRKYFLDV 121

QY 82 LESDLMQFKHISNNEYIIEDSFKILNSQKNTLKSYYKIKESVENDIKFAQEGISYSEK 141  
DB 122 LESDLMQFKHISNNEYIIEDSFKILNSQKNTLKSYYKIKESVENDIKFAQEGISYSEK 181  
QY 142 VLAKYKODLESIKKYIKKEKEKFPSSPTTPPSPAKTDQKESKFLPLTNIETLYNNL 201  
DB 182 VLAKYKODLESIKKYIKKEKEKFPSSPTTPPSPAKTDQKESKFLPLTNIETLYNNL 241  
QY 202 VNKIDYILINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLPKNPYDEAIKKLIND 261  
DB 242 VNKIDYILINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLPKNPYDEAIKKLIND 301  
QY 262 DTKDMLGKLISTGLVQNFPTTIISKLIEGKFQDMLNISQHCYVKQCPENSGCFRHLDE 321  
DB 302 DTKDMLGKLISTGLVQNFPTTIISKLIEGKFQDMLNISQHCYVKQCPENSGCFRHLDE 361  
QY 322 REECKCLLNYKQEGDKCVENPPTCNENNGGCDADATCTEEDSGSSRRKKITCECTKPDY 381  
DB 362 REECKCLLNYKQEGDKCVENPPTCNENNGGCDADATCTEEDSGSSRRKKITCECTKPDY 421  
QY 382 PLFDGIFCSS 391  
DB 422 PLFDGIFCSS 431

## RESULT 7

US-10-057-531A-1  
; Sequence 1, Application US/10057531A  
; Publication No. US20030161838A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyon, Jeffrey A.  
; APPLICANT: Angov, Evelina  
; TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite  
; TITLE OF INVENTION: Protein-142 Vaccine  
; FILE REFERENCE: 003/241/SAP  
; CURRENT APPLICATION NUMBER: US/10/057,531A  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/264,535  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/347,564  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 1  
; LENGTH: 546  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein  
; OTHER INFORMATION: Sequence in PET-Tx42  
US-10-057-531A-1

Query Match 97.0%; Score 2008.5; DB 4; Length 546;  
Best Local Similarity 89.5%; Pred. No. 3.6e-122;  
Matches 385; Conservative 0; Mismatches 4; Indels 41; Gaps 1;

QY 3 HHHHHHPGG-----SGSGTMAISV 21  
DB 117 HHHHHSSGLVPRGSGMKETAARKFERQHMDSPLDGTDDDDKAMADIGSIEGRGTMAISV 176  
QY 22 TMDNITLSGFENEYVYILKPLAGVYRSILKQIEKNIFFPNLNLNDILNSRLKKRYFLDV 81  
DB 177 TMDNITLSGFENEYVYILKPLAGVYRSILKQIEKNIFFPNLNLNDILNSRLKKRYFLDV 236  
QY 82 LESDLMQFKHISNNEYIIEDSFKILNSQKNTLKSYYKIKESVENDIKFAQEGISYSEK 141  
DB 237 LESDLMQFKHISNNEYIIEDSFKILNSQKNTLKSYYKIKESVENDIKFAQEGISYSEK 296  
QY 142 VLAKYKODLESIKKYIKKEKEKFPSSPTTPPSPAKTDQKESKFLPLTNIETLYNNL 201  
DB 297 VLAKYKODLESIKKYIKKEKEKFPSSPTTPPSPAKTDQKESKFLPLTNIETLYNNL 356

QY 202 VNKIDYILINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLPKNPYDEAIKKLIND 261  
DB 357 VNKIDYILINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLPKNPYDEAIKKLIND 416  
QY 262 DTKDMLGKLISTGLVQNFPTTIISKLIEGKFQDMLNISQHCYVKQCPENSGCFRHLDE 321  
DB 417 DTKDMLGKLISTGLVQNFPTTIISKLIEGKFQDMLNISQHCYVKQCPENSGCFRHLDE 476  
QY 322 REECKCLLNYKQEGDKCVENPPTCNENNGGCDADATCTEEDSGSSRRKKITCECTKPDY 381  
DB 477 REECKCLLNYKQEGDKCVENPPTCNENNGGCDADATCTEEDSGSSRRKKITCECTKPDY 536  
QY 382 PLFDGIFCSS 391  
DB 537 PLFDGIFCSS 546

## RESULT 8

US-10-057-532A-1  
; Sequence 1, Application US/10057532A  
; Publication No. US20030161839A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyon, Jeffrey A.  
; APPLICANT: Angov, Evelina  
; APPLICANT: Cohen, Joe D.  
; APPLICANT: Voss, Gerald  
; TITLE OF INVENTION: Recombinant P. falciparum Merozoite Protein-142 Vaccine  
; FILE REFERENCE: 003/238/SAP  
; CURRENT APPLICATION NUMBER: US/10/057,532A  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 60/264,535  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/347,564  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 1  
; LENGTH: 546  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein Sequence in I  
US-10-057-532A-1

Query Match 97.0%; Score 2008.5; DB 4; Length 546;  
Best Local Similarity 89.5%; Pred. No. 3.6e-122;  
Matches 385; Conservative 0; Mismatches 4; Indels 41; Gaps 1;

QY 3 HHHHHHPGG-----SGSGTMAISV 21  
DB 117 HHHHHSSGLVPRGSGMKETAARKFERQHMDSPLDGTDDDDKAMADIGSIEGRGTMAISV 176  
QY 22 TMDNITLSGFENEYVYILKPLAGVYRSILKQIEKNIFFPNLNLNDILNSRLKKRYFLDV 81  
DB 177 TMDNITLSGFENEYVYILKPLAGVYRSILKQIEKNIFFPNLNLNDILNSRLKKRYFLDV 236  
QY 82 LESDLMQFKHISNNEYIIEDSFKILNSQKNTLKSYYKIKESVENDIKFAQEGISYSEK 141  
DB 237 LESDLMQFKHISNNEYIIEDSFKILNSQKNTLKSYYKIKESVENDIKFAQEGISYSEK 296  
QY 142 VLAKYKODLESIKKYIKKEKEKFPSSPTTPPSPAKTDQKESKFLPLTNIETLYNNL 201  
DB 297 VLAKYKODLESIKKYIKKEKEKFPSSPTTPPSPAKTDQKESKFLPLTNIETLYNNL 356  
QY 202 VNKIDYILINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLPKNPYDEAIKKLIND 261  
DB 357 VNKIDYILINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLPKNPYDEAIKKLIND 416  
QY 262 DTKDMLGKLISTGLVQNFPTTIISKLIEGKFQDMLNISQHCYVKQCPENSGCFRHLDE 321  
DB 417 DTKDMLGKLISTGLVQNFPTTIISKLIEGKFQDMLNISQHCYVKQCPENSGCFRHLDE 476  
QY 322 REECKCLLNYKQEGDKCVENPPTCNENNGGCDADATCTEEDSGSSRRKKITCECTKPDY 381

Db 477 REECCLNLYKQEGDKVCVENPNTCNENNGCCDADATCTEEDSGSSRKKTCTECPDSSY 536  
QY 382 PLFDGIFCSS 391  
Db 537 PLFDGIFCSS 546

## RESULT 9

US-10-057-531A-5  
; Sequence 5, Application US/10057531A  
; Publication No. US20030161838A1  
; GENERAL INFORMATION:  
; APPLICANT: Angov, Jeffrey A.  
; APPLICANT: Lyon, Jeffrey A.  
; TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite  
; FILE REFERENCE: 003/241/SAP  
; CURRENT APPLICATION NUMBER: US/10/057,531A  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/264,535  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/347,564  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 5  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Plasmodium falciparum 3D7 MSP142  
US-10-057-531A-5

Query Match 95.0%; Score 1968; DB 4; Length 383;  
Best Local Similarity 99.2%; Pred. No. 1e-119;

Matches 376; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 GSGTMAISVTMDNIIISGFENEYDVYTLKPLAGVRSLLKKQIEKNIFTFNLNINDILNSRL 72  
Db 5 GRGTAISVTMDNIIISGFENEYDVYTLKPLAGVRSLLKKQIEKNIFTFNLNINDILNSRL 64  
QY 73 KKRKYFLDVLBSDLMOFPHISSNEYIIEDSFYTLNSSEKNTLLSKYKIKESVENDIKFA 132  
Db 65 KKRKYFLDVLBSDLMOFPHISSNEYIIEDSFYTLNSSEKNTLLSKYKIKESVENDIKFA 124  
QY 133 QEGISYERKVLAKYKDDLESIKVIKEEKEKPPSPPTTPSPAKTDEQKESKFLPLT 192  
Db 125 QEGISYERKVLAKYKDDLESIKVIKEEKEKPPSPPTTPSPAKTDEQKESKFLPLT 184  
QY 193 NIETLYNNLVNKIDYLLNLKAKINDCNVEKDEAHVKTITKLSDLKAIDKIDLFKNPYDF 252  
Db 185 NIETLYNNLVNKIDYLLNLKAKINDCNVEKDEAHVKTITKLSDLKAIDKIDLFKNPYDF 244  
QY 253 EAIKKLINDDTKKDMLGKLTSLGLVQNFNTIISKLIEGKFDMLNISQHCVKKQCPEN 312  
Db 245 EAIKKLINDDTKKDMLGKLTSLGLVQNFNTIISKLIEGKFDMLNISQHCVKKQCPEN 304  
QY 313 SGCFPHLDEREBCCKLLNLYKQEGDKVCVENPNTCNENNGCCDADATCTEEDSGSSRKKT 372  
Db 305 SGCFPHLDEREBCCKLLNLYKQEGDKVCVENPNTCNENNGCCDADATCTEEDSGSSRKKT 364  
QY 373 CECTKPDSSYPLFDGIFCSS 391  
Db 365 CECTKPDSSYPLFDGIFCSS 383

## RESULT 10

US-10-057-532A-5  
; Sequence 5, Application US/10057532A  
; Publication No. US20030161839A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyon, Jeffrey A.  
; APPLICANT: Angov, Evelina  
; APPLICANT: Cohen, Joe D.

; APPLICANT: Voss, Gerald  
; TITLE OF INVENTION: Recombinant P. falciparum Merozoite Protein-142 Vaccine  
; FILE REFERENCE: 003/238/SAP  
; CURRENT APPLICATION NUMBER: US/10/057,532A  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: US 60/264,535  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/347,564  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 5  
; LENGTH: 383  
; TYPE: PRT  
; ORGANISM: Plasmodium falciparum 3D7 MSP142  
US-10-057-532A-5

Query Match 95.0%; Score 1968; DB 4; Length 383;  
Best Local Similarity 99.2%; Pred. No. 1e-119;

Matches 376; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 GSGTMAISVTMDNIIISGFENEYDVYTLKPLAGVRSLLKKQIEKNIFTFNLNINDILNSRL 72  
Db 5 GRGTAISVTMDNIIISGFENEYDVYTLKPLAGVRSLLKKQIEKNIFTFNLNINDILNSRL 64  
QY 73 KKRKYFLDVLBSDLMOFPHISSNEYIIEDSFYTLNSSEKNTLLSKYKIKESVENDIKFA 132  
Db 65 KKRKYFLDVLBSDLMOFPHISSNEYIIEDSFYTLNSSEKNTLLSKYKIKESVENDIKFA 124  
QY 133 QEGISYERKVLAKYKDDLESIKVIKEEKEKPPSPPTTPSPAKTDEQKESKFLPLT 192  
Db 125 QEGISYERKVLAKYKDDLESIKVIKEEKEKPPSPPTTPSPAKTDEQKESKFLPLT 184  
QY 193 NIETLYNNLVNKIDYLLNLKAKINDCNVEKDEAHVKTITKLSDLKAIDKIDLFKNPYDF 252  
Db 185 NIETLYNNLVNKIDYLLNLKAKINDCNVEKDEAHVKTITKLSDLKAIDKIDLFKNPYDF 244  
QY 253 EAIKKLINDDTKKDMLGKLTSLGLVQNFNTIISKLIEGKFDMLNISQHCVKKQCPEN 312  
Db 245 EAIKKLINDDTKKDMLGKLTSLGLVQNFNTIISKLIEGKFDMLNISQHCVKKQCPEN 304  
QY 313 SGCFPHLDEREBCCKLLNLYKQEGDKVCVENPNTCNENNGCCDADATCTEEDSGSSRKKT 372  
Db 305 SGCFPHLDEREBCCKLLNLYKQEGDKVCVENPNTCNENNGCCDADATCTEEDSGSSRKKT 364  
QY 373 CECTKPDSSYPLFDGIFCSS 391  
Db 365 CECTKPDSSYPLFDGIFCSS 383

## RESULT 11

US-09-978-756-3  
; Sequence 3, Application US/09978756  
; Patent No. US20020160017A1  
; GENERAL INFORMATION:  
; APPLICANT: Holder, Anthony  
; APPLICANT: Birdsell, Betty  
; APPLICANT: Reaney, James  
; APPLICANT: Morgan, William  
; APPLICANT: Syed, Shabih  
; TITLE OF INVENTION: Malaria Vaccine  
; FILE REFERENCE: 18396/1005  
; CURRENT APPLICATION NUMBER: US/09/978,756  
; PRIOR FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: PCT/GB00/01558  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 09/311,817  
; PRIOR FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: 2,271,451  
; PRIOR FILING DATE: 1999-05-25  
; PRIOR APPLICATION NUMBER: 9909072.2  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.0  
; SEQ ID NO 3  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: plasmidium falciparum  
US-09-978-756-3

Query Match 94.9%; Score 1965; DB 3; Length 394;  
Best Local Similarity 100.0%; Pred. No. 1,66-119;  
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 18 AISTVMDNISGFENEVDYIYKPLAGYRSILKQIEKNIFFENINLNDIINSRLKGRKY 77
DB 1 AISTVMDNISGFENEVDYIYKPLAGYRSILKQIEKNIFFENINLNDIINSRLKGRKY 60
OY 78 FLDVLESQKQKHSNSNEYIIEDSFKLNSQKNTLLKSYKYIKESVENDIKFAQEGIS 137
DB 61 FLDVLESQKQKHSNSNEYIIEDSFKLNSQKNTLLKSYKYIKESVENDIKFAQEGIS 120
OY 138 YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDEOKKESKFLPLTNIETL 197
DB 121 YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDEOKKESKFLPLTNIETL 180
OY 198 YNNLVNKKIDVYLINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLFKNPYDEFAIKK 257
DB 181 YNNLVNKKIDVYLINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLFKNPYDEFAIKK 240
OY 258 LINDTKKDMGKILSTGLVONFPNTIISKLEGGFQDMINIISOHCYKQCPENSGGCFR 317
DB 241 LINDTKKDMGKILSTGLVONFPNTIISKLEGGFQDMINIISOHCYKQCPENSGGCFR 300
OY 318 HNDERECCCLNNTKQEGDKCVENPNPTCNENNGCGDADATCTEEDSGSSRKKITCECTK 377
DB 301 HNDERECCCLNNTKQEGDKCVENPNPTCNENNGCGDADATCTEEDSGSSRKKITCECTK 360
OY 378 PDSYPLFDGIFCSS 391
DB 361 PDSYPLFDGIFCSS 374
```

RESULT 12  
US-10-062-809-2  
; Sequence 2, Application US/10062809  
; Publication No. US20030100106A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Sandra P.  
; APPLICANT: Hashimoto, Ann  
; APPLICANT: Nishimura, Tani  
; TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMIDIUM FALCIPARUM VACCINE  
; FILE REFERENCE: A-67984-1/RFT/TAL/NBC  
; CURRENT APPLICATION NUMBER: US/10/062, 809  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/500, 376  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: US 60/266, 281  
; PRIOR FILING DATE: 2001-02-01  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: plasmidium falciparum  
US-10-062-809-2

Query Match 93.2%; Score 1931; DB 4; Length 394;  
Best Local Similarity 98.7%; Pred. No. 2,66-117;  
Matches 369; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
OY 18 AISTVMDNISGFENEVDYIYKPLAGYRSILKQIEKNIFFENINLNDIINSRLKGRKY 77
DB 1 AISTVMDNISGFENEVDYIYKPLAGYRSILKQIEKNIFFENINLNDIINSRLKGRKY 60
OY 78 FLDVLESQKQKHSNSNEYIIEDSFKLNSQKNTLLKSYKYIKESVENDIKFAQEGIS 137
```

```
DB 61 FLDVLESQKQKHSNSNEYIIEDSFKLNSQKNTLLKSYKYIKESVENDIKFAQEGIS 120
OY 138 YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDEOKKESKFLPLTNIETL 197
DB 121 YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDEOKKESKFLPLTNIETL 180
OY 198 YNNLVNKKIDVYLINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLFKNPYDEFAIKK 257
DB 181 YNNLVNKKIDVYLINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLFKNPYDEFAIKK 240
OY 258 LINDTKKDMGKILSTGLVONFPNTIISKLEGGFQDMINIISOHCYKQCPENSGGCFR 317
DB 241 LINDTKKDMGKILSTGLVONFPNTIISKLEGGFQDMINIISOHCYKQCPENSGGCFR 300
OY 318 HNDERECCCLNNTKQEGDKCVENPNPTCNENNGCGDADATCTEEDSGSSRKKITCECTK 377
DB 301 HNDERECCCLNNTKQEGDKCVENPNPTCNENNGCGDADATCTEEDSGSSRKKITCECTK 360
OY 378 PDSYPLFDGIFCSS 391
DB 361 PDSYPLFDGIFCSS 374
```

RESULT 13  
US-10-935-793-2  
; Sequence 2, Application US/10935793  
; Publication No. US20050037021A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Sandra P.  
; APPLICANT: Hashimoto, Ann  
; APPLICANT: Nishimura, Tani  
; TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMIDIUM FALCIPARUM VACCINE  
; FILE REFERENCE: A-67984-1/RFT/TAL/NBC  
; CURRENT APPLICATION NUMBER: US/10/935, 793  
; CURRENT FILING DATE: 2004-09-07  
; PRIOR APPLICATION NUMBER: US/10/062, 809  
; PRIOR FILING DATE: 2002-02-01  
; PRIOR APPLICATION NUMBER: US 09/500, 376  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: US 60/266, 281  
; PRIOR FILING DATE: 2001-02-01  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: plasmidium falciparum  
US-10-935-793-2

Query Match 93.2%; Score 1931; DB 5; Length 394;  
Best Local Similarity 98.7%; Pred. No. 2,66-117;  
Matches 369; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
OY 18 AISTVMDNISGFENEVDYIYKPLAGYRSILKQIEKNIFFENINLNDIINSRLKGRKY 77
DB 1 AISTVMDNISGFENEVDYIYKPLAGYRSILKQIEKNIFFENINLNDIINSRLKGRKY 60
OY 78 FLDVLESQKQKHSNSNEYIIEDSFKLNSQKNTLLKSYKYIKESVENDIKFAQEGIS 137
DB 61 FLDVLESQKQKHSNSNEYIIEDSFKLNSQKNTLLKSYKYIKESVENDIKFAQEGIS 120
OY 138 YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDEOKKESKFLPLTNIETL 197
DB 121 YYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDEOKKESKFLPLTNIETL 180
OY 198 YNNLVNKKIDVYLINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLFKNPYDEFAIKK 257
DB 181 YNNLVNKKIDVYLINLAKINDCNVEKDEAHVKITKLSDLKAIIDKIDLFKNPYDEFAIKK 240
OY 258 LINDTKKDMGKILSTGLVONFPNTIISKLEGGFQDMINIISOHCYKQCPENSGGCFR 317
DB 241 LINDTKKDMGKILSTGLVONFPNTIISKLEGGFQDMINIISOHCYKQCPENSGGCFR 300
```



QY 318 HDEREBCCKLNTYKQBGKCVENPNTCNENNGGCDADATCTEEDSGSSRKKITCECTK 377  
DB 301 HDEREBCCKLNTYKQBGKCVENPNTCNENNGGCDADAKCTEEDSGSNGKKITCECTK 360  
QY 378 PDSYPLFDGIFCSS 391  
DB 361 PDSYPLFDGIFCSS 374

## RESULT 14

US-10-925-385-2  
; Sequence 2, Application US/10925385  
; Publication No. US20050095255A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Sandra P.  
; APPLICANT: Kramer, Kenton J.  
; APPLICANT: Goshell, William J.  
; APPLICANT: Nishimura, Tani  
; TITLE OF INVENTION: Baculovirus Produced Plasmodium Falciiparum Vaccine  
; FILE REFERENCE: A-67984-2  
; CURRENT APPLICATION NUMBER: US/10/925,385  
; CURRENT FILING DATE: 2004-08-24  
; PRIOR APPLICATION NUMBER: US 09/500,376  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: US 08/195,705  
; PRIOR FILING DATE: 1994-02-14  
; PRIOR APPLICATION NUMBER: US 07/867,768  
; PRIOR FILING DATE: 1992-04-13  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 394  
; TYPE: PRT  
; ORGANISM: plasmodium falciiparum  
US-10-925-385-2

Query Match 93.2%; Score 1911; DB 5; Length 394;  
Best Local Similarity 98.7%; Pred. No. 2, 6e-117;

Matches 369; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 18 AISTVMDNLSGFENEYDVIYLLKPLAGVYRSLLKQIEKNIPTFNLNDLINSRLKKRY 77  
DB 1 AISTVMDNLSGFENEYDVIYLLKPLAGVYRSLLKQIEKNIPTFNLNDLINSRLKKRY 60  
QY 78 FLVDLESMDLMOFKHISSENYIIEDSFKLNSBQKNTLLSKYIKESVENDIKFAQBG 137  
DB 61 FLVDLESMDLMOFKHISSENYIIEDSFKLNSBQKNTLLSKYIKESVENDIKFAQBG 120  
QY 138 YYEKVLAKYKDDLESIKKYIKEKEKFPSSPTTPSPAKTDEQKESKFLPLTNIE 197  
DB 121 YYEKVLAKYKDDLESIKKYIKEKEKFPSSPTTPSPAKTDEQKESKFLPLTNIE 180  
QY 198 YNNLVNKKIDYLLINKAKINDCNVEKDEAHVKITKLSDLKAIIDDKIDLFKNHDPFAI 257  
DB 181 YNNLVNKKIDYLLINKAKINDCNVEKDEAHVKITKLSDLKAIIDDKIDLFKNHDPFAI 240  
QY 258 LINDTKKMDLGLSTGLVQNFPTIISKLEIGKQDMNLINSOHCQCVKQCPENSGC 317  
DB 241 LINDTKKMDLGLSTGLVQNFPTIISKLEIGKQDMNLINSOHCQCVKQCPENSGC 300  
QY 318 HDEREBCCKLNTYKQBGKCVENPNTCNENNGGCDADATCTEEDSGSSRKKITCECTK 377  
DB 301 HDEREBCCKLNTYKQBGKCVENPNTCNENNGGCDADAKCTEEDSGSNGKKITCECTK 360  
QY 378 PDSYPLFDGIFCSS 391  
DB 361 PDSYPLFDGIFCSS 374

RESULT 15  
US-10-062-809-18  
; Sequence 18, Application US/10062809

; Publication No. US20030100106A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Sandra P.  
; APPLICANT: Hashimoto, Ann  
; APPLICANT: Nishimura, Tani  
; TITLE OF INVENTION: BACULOVIRUS PRODUCED PLASMODIUM FALCIPARUM VACCINE  
; FILE REFERENCE: A-67984-1/RFT/TAI/NBC  
; CURRENT APPLICATION NUMBER: US/10/062,809  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/500,376  
; PRIOR FILING DATE: 2000-02-08  
; PRIOR APPLICATION NUMBER: US 60/266,281  
; PRIOR FILING DATE: 2001-02-01  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-062-809-18

Query Match 93.1%; Score 1928; DB 4; Length 396;  
Best Local Similarity 98.1%; Pred. No. 4, 1e-117;  
Matches 368; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 16 TMAISVTMDNLSGFENEYDVIYLLKPLAGVYRSLLKQIEKNIPTFNLNDLINSRLKKR 75  
DB 20 TMAISVTMDNLSGFENEYDVIYLLKPLAGVYRSLLKQIEKNIPTFNLNDLINSRLKKR 79  
QY 76 KYFLDLESMDLMOFKHISSENYIIEDSFKLNSBQKNTLLSKYIKESVENDIKFAQBG 135  
DB 80 KYFLDLESMDLMOFKHISSENYIIEDSFKLNSBQKNTLLSKYIKESVENDIKFAQBG 139  
QY 136 ISYEKVLAKYKDDLESIKKYIKEKEKFPSSPTTPSPAKTDEQKESKFLPLTNIE 195  
DB 140 ISYEKVLAKYKDDLESIKKYIKEKEKFPSSPTTPSPAKTDEQKESKFLPLTNIE 199  
QY 156 TLNNLVNKKIDYLLINKAKINDCNVEKDEAHVKITKLSDLKAIIDDKIDLFKNHDPFAI 255  
DB 200 TLNNLVNKKIDYLLINKAKINDCNVEKDEAHVKITKLSDLKAIIDDKIDLFKNHDPFAI 259  
QY 256 KKLINDTKKMDLGLSTGLVQNFPTIISKLEIGKQDMNLINSOHCQCVKQCPENSGC 315  
DB 260 KKLINDTKKMDLGLSTGLVQNFPTIISKLEIGKQDMNLINSOHCQCVKQCPENSGC 319  
QY 316 FRLHDEREBCCKLNTYKQBGKCVENPNTCNENNGGCDADATCTEEDSGSSRKKITCEC 375  
DB 320 FRLHDEREBCCKLNTYKQBGKCVENPNTCNENNGGCDADAKCTEEDSGSNGKKITCEC 379  
QY 376 TKPDSYPLFDGIFCS 390  
DB 380 TKPDSYPLFDGIFCS 394

Search completed: May 5, 2006, 00:29:05  
Job time : 169 secs

**THIS PAGE IS BLANK**



QY	202	UNKIDYLLINAKINDCNVEDQEAHVKTTRLSDKALDGDYIDTFRNPYDEALFKKIND	261
Db	202	VSXKNTYTTDMKLVINNCQLEKKEKELTYKKLDQYNNRDKLEIK-----KSKK--NE	254
QY	262	DTKKDMGKLLSTGLV-QNFPNTTISKLEIGKFDMLNISQHCYKQCPENSGCFRHL	320
Db	255	VKSSGELLEKMSKLIKENESKEILLSQLNLVQTLLTWSSSEHTCIDTNVPDNNACYRHL	314
QY	321	EREBCKCLNMYKQEGKXCVENPPTCNENNGCCDADCTEEDSSSKKTTCTCTPDS	380
Db	315	GTEEMWCLLTFKEBGGKCVSPASNVTCDDNNGGCAEACKMTDS---NKIVCKTKEGS	370
QY	381	YPLFDGIKPS	390
Db	371	EPLEBGVFC	380

## RESULT 2

```

US-11-144-833-13
; Sequence 13, Application US/11144833
; Publication No. US20060018932A1
; GENERAL INFORMATION:
; APPLICANT: LONGACRE-ANDRE, SHIRLEY
; APPLICANT: ROTH, CHARLES
; APPLICANT: NATO, FARIDABANO
; APPLICANT: BARNWELL, JOHN
; APPLICANT: MENDIS, KAMINI
; TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT
; TITLE OF INVENTION: OF PLASMODIUM MSP-1
; FILE REFERENCE: 0660-0139-0XPT
; CURRENT APPLICATION NUMBER: US/11/144, 833
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US/09/125,031
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: PCT/FR97/00290
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: FR96/01822
; PRIOR FILING DATE: 1996-02-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Plasmodium vivax-like sp.
; US-11-144-833-13

```

[illegible]

Db 304 PDNAACYRLIDGTEENKRLITFKBEGGKCVASNTCTDNNGGCAPPEAECMTDS-----N 355  
 QY 370 KINCECTKPDSPPLPDGIFCS 390  
 |||:||||| |||:|||||  
 Db 360 KIVCKCTKBSGSEPLFEGVFCFS 380

RESULT 3  
US-11-144-833-11

```

? Sequence 11, Application US/11/144833
? Publication No. US20060018932A1
? GENERAL INFORMATION:
? APPLICANT: LONGACRE-ANDRE, SHIRLEY
? APPLICANT: ROTH, CHARLES
? APPLICANT: NATO, FARIDABANO
? APPLICANT: BARNWELL, JOHN
? APPLICANT: MENDIS, KAMINI
? TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT
? TITLE OF INVENTION: OF PLASMODIUM MSP-1
? FILE REFERENCE: 0660-0139-0XPCT
? CURRENT APPLICATION NUMBER: US/11/144,833
? PRIOR FILING DATE: 2005-06-06
? PRIOR APPLICATION NUMBER: US/09/125,031
? PRIOR FILING DATE: 1999-03-10
? PRIOR APPLICATION NUMBER: PCT/FR77/00290
? PRIOR FILING DATE: 1997-02-14
? PRIOR APPLICATION NUMBER: FR96/01822
? PRIOR FILING DATE: 1996-02-14
? NUMBER OF SEQ ID NOS: 15
? SOFTWARE: Patentin version 3.1
? SEQ ID NO 11
? LENGTH: 379
? TYPE: PRT
? ORGANISM: Plasmodium cynomolgi
? US-11-144-833-11

```

Query Match	35.5%	Score 734.5	DB 11	Length 379
Best Local Similarity	41.9%	Pred. No. 26-36		
Matches 156; Conservative	74;	Mismatches 115;	Indels 27;	Gaps 10;

[illegible]

## RESULT 4

US-11-144-833-10  
; Sequence 10, Application US/11144833  
; Publication No. US20060018932A1

GENERAL INFORMATION:  
APPLICANT: LONGACRE-ANDRE, SHIRLEY  
APPLICANT: ROTH, CHARLES  
APPLICANT: NATO, FARIDABANO  
APPLICANT: BARNWELL, JOHN  
APPLICANT: MENDIS, KAMINI  
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT  
FILE REFERENCE: 0660-0139-0XPCT  
CURRENT APPLICATION NUMBER: US/11/144,833  
CURRENT FILING DATE: 2005-06-06  
PRIOR APPLICATION NUMBER: US/09/125,031  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: PCT/FR97/00290  
PRIOR FILING DATE: 1997-02-14  
PRIOR APPLICATION NUMBER: FR96/01822  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Plasmodium falciparum  
US-11-144-833-10

Query Match 25.4%; Score 527; DB 11; Length 108;  
Best Local Similarity 94.8%; Pred. No. 7, 8e-25;  
Matches 91; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 295 DMLNISOHCYKQCPENSGCFRHLDERECKCLNTNYKQEDKCVENPPTCNENNGGCD 354  
DB 13 DFNISQHCYKQCPENSGCFRHLDERECKCLNTNYKQEDKCVENPPTCNENNGGCD 72

QY 355 ADATTEEDSGSSRKKTCTECPDPSYPLFDGIFCS 390  
DB 73 ADAKTEEDSGSGKKTCTECPDPSYPLFDGIFCS 108

RESULT 5  
US-11-144-833-5  
Sequence 5, Application US/11/144833  
Publication No. US20060018932A1  
GENERAL INFORMATION:  
APPLICANT: LONGACRE-ANDRE, SHIRLEY  
APPLICANT: ROTH, CHARLES  
APPLICANT: NATO, FARIDABANO  
APPLICANT: BARNWELL, JOHN  
APPLICANT: MENDIS, KAMINI  
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT  
FILE REFERENCE: 0660-0139-0XPCT  
CURRENT APPLICATION NUMBER: US/11/144,833  
CURRENT FILING DATE: 2005-06-06  
PRIOR APPLICATION NUMBER: US/09/125,031  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: PCT/FR97/00290  
PRIOR FILING DATE: 1997-02-14  
PRIOR APPLICATION NUMBER: FR96/01822  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-11-144-833-5

Query Match 25.4%; Score 527; DB 11; Length 116;  
Best Local Similarity 96.8%; Pred. No. 8, 5e-25;  
Matches 91; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 298 NISOHCYKQCPENSGCFRHLDERECKCLNTNYKQEDKCVENPPTCNENNGGCDADA 357  
DB 3 NISOHCYKQCPENSGCFRHLDERECKCLNTNYKQEDKCVENPPTCNENNGGCDADA 62  
QY 358 TCTEEDSGSSRKKTCTECPDPSYPLFDGIFCS 391  
DB 63 KCTEEDSGSGKKTCTECPDPSYPLFDGIFCS 96

RESULT 6  
US-11-144-833-2  
Sequence 2, Application US/11/144833  
Publication No. US20060018932A1  
GENERAL INFORMATION:  
APPLICANT: LONGACRE-ANDRE, SHIRLEY  
APPLICANT: ROTH, CHARLES  
APPLICANT: NATO, FARIDABANO  
APPLICANT: BARNWELL, JOHN  
APPLICANT: MENDIS, KAMINI  
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT  
FILE REFERENCE: 0660-0139-0XPCT  
CURRENT APPLICATION NUMBER: US/11/144,833  
CURRENT FILING DATE: 2005-06-06  
PRIOR APPLICATION NUMBER: US/09/125,031  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: PCT/FR97/00290  
PRIOR FILING DATE: 1997-02-14  
PRIOR APPLICATION NUMBER: FR96/01822  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 95  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-11-144-833-2

Query Match 25.3%; Score 523; DB 11; Length 95;  
Best Local Similarity 96.8%; Pred. No. 1, 2e-24;  
Matches 90; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 298 NISOHCYKQCPENSGCFRHLDERECKCLNTNYKQEDKCVENPPTCNENNGGCDADA 357  
DB 3 NISOHCYKQCPENSGCFRHLDERECKCLNTNYKQEDKCVENPPTCNENNGGCDADA 62

QY 358 TCTEEDSGSSRKKTCTECPDPSYPLFDGIFCS 390  
DB 63 KCTEEDSGSGKKTCTECPDPSYPLFDGIFCS 95

RESULT 7  
US-11-144-833-8  
Sequence 8, Application US/11/144833  
Publication No. US20060018932A1  
GENERAL INFORMATION:  
APPLICANT: LONGACRE-ANDRE, SHIRLEY  
APPLICANT: ROTH, CHARLES  
APPLICANT: NATO, FARIDABANO  
APPLICANT: BARNWELL, JOHN  
APPLICANT: MENDIS, KAMINI  
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT  
FILE REFERENCE: 0660-0139-0XPCT  
CURRENT APPLICATION NUMBER: US/11/144,833  
CURRENT FILING DATE: 2005-06-06  
PRIOR APPLICATION NUMBER: US/09/125,031  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: PCT/FR97/00290  
PRIOR FILING DATE: 1997-02-14  
PRIOR APPLICATION NUMBER: FR96/01822

PRIOR FILING DATE: 1996-02-14  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patent version 3.1  
SEQ ID NO 8  
LENGTH: 127  
TYPE: PRT  
ORGANISM: Plasmodium falciparum  
US-11-144-833-8

Query Match 25.3%; Score 523; DB 11; Length 127;  
Best Local Similarity 96.8%; Pred. No. 1.6e-24;  
Matches 90; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

298 NISQHCYKQCPENSGCFRHLDEREBCCLNLYKQEGDKCVENPNPTCNENGGCDADA 357  
DB 35 NISQHCYKQCPENSGCFRHLDEREBCCLNLYKQEGDKCVENPNPTCNENGGCDADA 94  
QY 358 TCTEEDSGSSRRKKTCTCTKPDSPYLPDGI FCS 390  
DB 95 KCTEEDSGSGNGKKTCTCTKPDSPYLPDGI FCS 127

RESULT 8  
US-11-144-833-14

Sequence 14, Application US/11144833  
Publication No. US20060018932A1  
GENERAL INFORMATION:  
APPLICANT: LONGACRE-ANDRE, SHIRLEY  
APPLICANT: ROTH, CHARLES  
APPLICANT: NATO, FARIDABANO  
APPLICANT: BARNWELL, JOHN  
APPLICANT: MENDIS, KAMINI  
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT  
FILE REFERENCE: 0660-0139-0XPCOT  
CURRENT FILING DATE: 2005-06-06  
PRIOR FILING DATE: 2005-06-06  
PRIOR FILING DATE: 1999-03-10  
PRIOR FILING DATE: 1997-02-14  
PRIOR APPLICATION NUMBER: PCT/FR97/00290  
PRIOR FILING DATE: 1996-02-14  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patent version 3.1  
SEQ ID NO 14  
LENGTH: 281  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-11-144-833-14

Query Match 20.5%; Score 424.5; DB 11; Length 281;  
Best Local Similarity 35.7%; Pred. No. 2.7e-18;  
Matches 131; Conservative 55; Mismatches 66; Indels 115; Gaps 25;

QY 34 YDVTLLKLAGYVRSLKQIEKNITFTNINLN-DIINSLRKKRYFLDVLESDDLQFQHI 92  
DB 20 YDVTLLKLAGYVRSLKQIEKNITFTNINLN-DIINSLRKKRYFLDVLESDDLQFQHI 68  
QY 93 SSNEEYIIDSFKLLSEQKNTLLKSKYIKESVENDIKFAOEGISYEKVLAKYDDLES 152  
DB 69 PSGETIICDPTLLLEKKK-LGSYKYGASDDI-ANDG-YTKMGLYKH----- 114  
QY 153 IKKVIKEKEKFPSSPPTTPSPAKTDEQKESKFLPFLTNIETL--YNNLVNKIDYLL 209  
DB 115 --LVKVEID-----KKGRKAKELKFLPSQKELYLVKYVTDL----- 149  
QY 210 INLAKINDCNVEKDEAHVKTITKLSDLKAIIDKID-LFKNPYDPFAIKKLINDDTKXML 268  
DB 150 ---KKINNCOEKKEV-----KLDYKMDLYKS----- 174

QY 269 GKULSTGLVQNPFTIISKLEIGKFOMLNI-----SQHCYKQCPENSGCFRHLDERE 323  
DB 175 KVVSSGSLER-----LMSKLTIESKL-SLNVOTQLMSEHCIDTNPV-NAACYRYLDGTE 227  
QY 324 ECKCLNLYKQEGDKCVENPNPTCNENGGCDADATCTEEDSGSSRRKKTCTCTKPDSPYLP 383  
DB 228 EMRCLL-FKE--GKCV--PANTC-KDNGGCAPEACEKMDN-----IVCKCTEGSEPL 274  
QY 384 FDGI FCS 390  
DB 275 FBGV FCS 281

RESULT 9  
US-11-037-243-65

Sequence 65, Application US/11037243  
Publication No. US20050287546A1  
GENERAL INFORMATION:  
APPLICANT: PLOWMAN, GREGORY  
APPLICANT: WHYTE, DAVID  
APPLICANT: CAENEPEEL, SEAN  
APPLICANT: CHARVOCZAK, GLEN  
APPLICANT: MANNING, GERARD  
APPLICANT: SUDARSANAM, SUCHA  
TITLE OF INVENTION: NOVEL PROTEASES  
FILE REFERENCE: 038602/1214  
CURRENT FILING DATE: 2005-05-26  
PRIOR FILING DATE: 2005-09-26  
PRIOR FILING DATE: 2001-06-26  
PRIOR FILING DATE: 2000-06-26  
NUMBER OF SEQ ID NOS: 150  
SOFTWARE: Patent ver. 2.1  
SEQ ID NO 65  
LENGTH: 980  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-037-243-65

Query Match 6.8%; Score 140.5; DB 11; Length 980;  
Best Local Similarity 20.9%; Pred. No. 0.7;  
Matches 77; Conservative 64; Mismatches 154; Indels 73; Gaps 15;

QY 27 LSGFENEYDVYLLPLAGVYRSLKQIEKNITFTNINLN-DIINSLRKKRYFLDVLESDDL 86  
DB 341 LQFSNUGNTCYM-----NALIQSLFSLQSPANDLLKQIGIPWKITPLNAL--I 386  
QY 87 MOPKHSISEEYIIDSFKLLSEQKNTLLKSKYIKESVENDIKFAOEGISY----- 139  
DB 387 RRPFLHLVKK-----DINSETRKDLLK-----KVKAIAISATABRFSGQMNDANE 432  
QY 140 --EYVLAKYKDDLESIKKVIKEKEKFPSSPPTTPSPAKTDEQKESKFLPFLTNIET 196  
DB 433 FLSCLOQLDKEMKLNKTWTTEPVSGEENBPDISATRAVY-----CPVITNLEFE 483  
QY 197 LNNLVNKIDYLLINLAKINDCNVEKDEAHVKTITKLSDLKAIIDKIDLFKNPYDPF-AI 255  
DB 484 VOHSITCAGEIIPKKEQFPNDLSIDLPKRPKLP-----RSIDSDSLFPRAELELEVS 539  
QY 310 PENS-----GCFRHLDEREBCCLNLYKQEGDKCVENPN-PTCNENGGCDADATCTEE 362  
DB 540 ECKGKCALVRH--KFNRLPRLVILHLKRYGFVALS--LNNKIGQGVIIIPRYLTLSHC 595  
QY 596 TENKTPPTLQMSAHMAMSRPLKA-----SQMVNSCTSPSPSKKFTFKSKSLALCDS 651  
DB 363 DSGSSRRK 370  
DB 652 DSEDELK 659

RESULT 10  
US-10-793-626-2964  
; Sequence 2964, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMBERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PUS48005  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2964  
; LENGTH: 5024  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (5024)  
; OTHER INFORMATION: variable amino acid  
US-10-793-626-2964

Query Match 6.4%; Score 133; DB 9; Length 5024;  
Best Local Similarity 24.2%; Pred. No. 14;  
Matches 68; Conservative 49; Mismatches 126; Indels 38; Gaps 10;  
QY 46 YRSKKQIE---KNIFTPNLNDILNSRLKKRYFLDYL--SDLMQFKHSSNEVIE 100  
DB 1445 YNNAAKQAEIDINNSNPNLNAQDITNA-LNNIKQAQDYLHQAQLQDQK--TTQAI-- 1470  
QY 101 DSFKLNSQKNTLLSKYKIKESVENDIKFAQEGISYKYELARYKDDLESIKKVIKEE 160  
DB 1471 GNLNLNPQKDALIQ-----AINGATSRDQVAEKLK--BAEALDEAMKQL 1514  
QY 161 KEKFPSSPTTPSPAKTDEQKESKFLPFLNIEFLYNNLVN-----KIDYILNLKA 214  
DB 1515 EDQVNOQDOISNSPFIENSDQKTYNDKIQAAKEIINQTSNPTLDKQKADTLQNTKD 1574  
QY 215 KINQCNVEDEAHVKITKLSDKAIDDKIDLFKNPYDFAIKKLINDPTKDKMLGKLST 274  
DB 1575 AVNNHGGQKLAQSQDANQNLHDDLTBEQKNHF-----KPLINNADTRDEVNKKQLEI 1629  
QY 275 GLVONFPNTIISKLEIGK--FQDMNLNISQHCVCVKQCPENS 313  
DB 1630 AKQNLGDMSTLHKVINDKDQIQHLSNYINADNDKQYNDNA 1670

RESULT 11  
US-10-240-771A-2  
; Sequence 2, Application US/10240771A  
; Publication No. US20060036074A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; TITLE OF INVENTION: New protein with polybromo domains  
; FILE REFERENCE: hupolybromolcbws  
; CURRENT APPLICATION NUMBER: US/10/240,771A  
; CURRENT FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1633  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-240-771A-2

Query Match 6.1%; Score 126.5; DB 9; Length 1633;  
Best Local Similarity 20.1%; Pred. No. 8.7;  
Matches 66; Conservative 63; Mismatches 104; Indels 95; Gaps 17;

QY 48 SIKQIEKNIFTPNLNDILNSRLKKRYFLD-VLES-----DLMQFKHSSNE 96  
DB 507 SAKRSKKNI-----RKQRMKILFNVLLEAREPSGRRLDLPVVKP-SKDD 552  
QY 97 YIIEDSFKLNSQKNTLLSKYKIKESVENDIKFAQEGI-----SYEKVLAK 145  
DB 553 Y--PDYVKIIEPM-----DLKIIENHNRNDKVGAGEGMIIDMKLFNANHYNEEGSQ 604  
QY 146 YKDDLESIKVIEKEK--FPSSPTTPPS---PAKTDEQKESKFL--PFLNIEFLY 198  
DB 605 VYNDHILKELKEKKEKELGPLDDDMASPKLSRSKSGISPKSKTYWTPMOQLNEVY 664  
QY 199 NNLVANKID-----DYLNLKAKINDCNVEKDEAHVKITKLSDKA 238  
DB 665 EAVKNYTDKGRRLSAIFLRLPSESLDYITLIKPM---DMKIRSHMANNTKQDIDS 721  
QY 239 -IDDKIDLFKNPYDFAIKKLIND-----TKQDMGLKSLSTGLVONFPNT--II 285  
DB 722 WVEDEPMVFNNACTYNEPESLYKDALVHLKVILETTRDLEDGEDS-----HVPVTLII 776  
QY 266 SKLIEGKFQDMNLNISQHCVCVKQCPENS 313  
DB 777 QELHNLFP--VSVMSHODDEGRGYSDS 801

RESULT 12  
US-11-087-099-10455  
; Sequence 10455, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 10455  
; LENGTH: 807  
; TYPE: PRT  
; ORGANISM: Helicobacter pylori  
US-11-087-099-10455

Query Match 6.1%; Score 126; DB 11; Length 807;  
Best Local Similarity 22.2%; Pred. No. 4;  
Matches 88; Conservative 69; Mismatches 119; Indels 120; Gaps 23;

QY 50 KKQIEKNIFTPNLNDILNSRL--KKRYFLDV--LESMLQFKH-----SSN 95  
DB 147 RKLEQGV-----LDCLNNAKTDERKKCLDKLPKDLQSDILAKESVKAAYKDCVSAQAN 200  
QY 96 EYIIEDSFKLNSQKNTLLSKYKIKESVENDIKFAQEGISYKYELARYKDDLE---- 151  
DB 201 EAEKKECEKLLTPEAK-----KLEEBE-----AKESVKAAYLDCVSAQTEAEKKEC 246  
QY 152 -----SIKVIKKE--KEKFPSSPTTPSPAKTDEQKESKFLPFLNIEFLYNNLVNK 204  
DB 247 EKLTPKAKKLIBEAKESVKAAYLDCV--SQAKTEAEKKECEK-----LTPEAKK 296  
QY 205 IDYILNLKAKINDC-----NVEKDEAHVKIT--KLSDKAIDDKIDLFKNPYDFA 254  
DB 297 LBEAKSVKAYL-DCVSAQTEDEKECEKLLTPEARKLLEQQA---LDCLNNAKTDEE 351  
QY 255 IKKLINDPTKDKMLKSLSTGLVONFPNTIISKLEIGKFQDMNLNISQHCVCVKQCPENS 309  
DB 352 RKKCLK-DLPKDLQKVLAKESVK-----AYLDCVSAQKAEKKECEKLLT 397  
QY 310 PE-----NSGCF---RHLDRECKCLLVYKQEGKCVENPNPTCNENNNG 352  
DB 398 PEARKLIBEAKESVKAAYLDCVSKANKEKKECEKLLT--PEAKKLE-----BEAKES 449  
QY 353 CDADATCTEEDSGSRKKITCECTK--PDSYPLFD 385

Db 450 VKAYLDCVSOAKTEAEK--ECEKLLTPPEAKKLE 482

RESULT 13

US-11-096-568A-29300

; Sequence 29300, Application US/11096568A

; Publication No. US20060048240A1

; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nickolai et al.

; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides

; TITLE OF INVENTION: Methyl

; FILE REFERENCE: 2750-1592PUS2

; CURRENT APPLICATION NUMBER: US/11/096,568A

; CURRENT FILING DATE: 2005-04-01

; NUMBER OF SEQ ID NOS: 34471

; SEQ ID NO 29300

; LENGTH: 1054

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(1054)

; OTHER INFORMATION: Ceres Seq. ID no. 4808407

US-11-096-568A-29300

Query Match 6.1%; Score 126; DB 11; Length 1054;

Best Local Similarity 18.9%; Pred. No. 5.5;

Matches 77; Conservative 80; Mismatches 142; Indels 108; Gaps 19;

QY 50 KKQIEKNITFT---NLNLNDILNSRLKRRKFLDVLSDLMQFQHSNEYIIEDSKL 105

DB 10 KKAASDKSLIVDSADASHQIDKSAIKKPKY---VQISVQYTHFTG---LBEQIKS 61

QY 106 LNSEOK--NTLLKSKYIKESVENDIKFAQEGSYEYKVLAKYKODLSIKVIEKEXK 163

DB 62 YDVQIKGYDVQVQYKTEYNOVESYEOVKPEGOIDAVDEYHEVEQVQKLNDEVDLNEK 121

QY 164 FPPSPPTTPPPAKTDEQK-----ESKFLPLTNIETLYNNLVNKI--DDYLNTL 212

DB 122 LSVANBEITKALVKQSHKVAEDAVSGWEKADAEMLAKNTLESYTSLSKLAEDRAHL 181

QY 213 KAKINDC---NVEKD-EAAVYKTKLSLKLAI-----DDKIDLFKNPYDEA 254

DB 182 DGALECKRKQIRNLKKDEVLKLDVALSKTKQIEKMTMEFEKRMCDYEOELRSADSDA 241

QY 255 IKKLINDPTKKMLKLT-----LSTGLVQ-----NPTVTISKLEIGKF 293

DB 242 LSRTLQEE-RSMVLVYKSEKSRADAEIETLSNLEMCEREIKSLKIEYHVVSKLE--- 296

QY 294 QDMLNISQHCYKQCPENSGCFRLDE-----RECKCLLNYKQEGDKCVENPNPTC 346

DB 297 --IRREKKNMCRISMSANIK---QHLEGVKTIKALEBQGRRLSLVRK-----KLPGPA 346

QY 347 -----NENNGCCADATCTEEDSGSSRK---KITCECTKPPSY 381

DB 347 LAQMKLEVENLG-----RDSGDARQKRSYKVSPPCKSPGAY 383

US-11-096-568A-29300

RESULT 14

US-10-793-626-1358

; Sequence 1358, Application US/10793626

; Publication No. US20050255478A1

; GENERAL INFORMATION:

; APPLICANT: KIMMERLY, WILLIAM JOHN

; TITLE OF INVENTION: STRAPHLOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

; FILE REFERENCE: PUS4800S

; CURRENT APPLICATION NUMBER: US/10/793,626

; CURRENT FILING DATE: 2004-03-04

; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 4472

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

US-10-793-626-1358

; LENGTH: 583

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: amino acid sequence

US-10-793-626-1358

Query Match 6.1%; Score 125.5; DB 9; Length 583;

Best Local Similarity 22.3%; Pred. No. 2.9;

Matches 52; Conservative 42; Mismatches 84; Indels 55; Gaps 8;

QY 46 YRSLKQIEKNITFTNNLNDI--LNSRLKRRKFLDVLSDLMQFQHSNEY--IIED 101

DB 340 YHNEIKGFQKQLEHLSTRENEITOFNQYLEKQVFNQLD-----KIISYQKPIVEE 393

QY 102 SFKLNSQKNTLKSYYIKESVENDIKFAQEGSYEYKVLAKYKODLSIKVIEKEXK 161

DB 394 EIKRLYSEYNDLITKEELTEKMNKNKQFA-----IIEHYTEIYKLKIIDE-- 442

QY 162 EKFPSPPTTPPPAKTDEQKESKFLPLTNIETLY-----NLVKNKIDVYLINLKA 214

DB 443 -----SERQKDEKLPDKQLDKSSYLSKLEKKEKQLEIESTITNIDA 486

QY 215 KINCQNEKDEAHVYKTKLSLKLAIIDKIDLFKNP-----YFPEAIKILIN 260

DB 487 TLIDLNDKDD---FVNEIKSAMSIGDPCIGNEIHSIGEHIDFESIAQRNN 535

US-11-087-099-5472

RESULT 15

US-11-087-099-5472

; Sequence 5472, Application US/11087099

; Publication No. US20060041961A1

; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53450)B EP

; CURRENT APPLICATION NUMBER: US/11/087,099

; CURRENT FILING DATE: 2005-03-22

; NUMBER OF SEQ ID NOS: 12464

; SEQ ID NO 5472

; LENGTH: 1927

; TYPE: PRT

; ORGANISM: Helicobacter pylori 26695

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)-(1927)

; OTHER INFORMATION: unsure at all Xaa locations

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472

US-11-087-099-5472





**THIS PAGE BLANK (USPTO)**

CC 1(42) protein was produced as a soluble protein in *Escherichia coli* host

cell cytoplasm by manipulation of IPTG concentration and induction temperature. MSP-1(42) was purified to greater than 95% purity, and showed immunoreactivity with anti-MSP-1 antibodies. It was stable when stored for 18 months at -80 degrees C. The invention relates to the production of large amounts of MSP-1(42) which maintain conformational epitopes critical for development of vaccines. The vaccines are useful against malaria or for eliciting immune responses against *P. falciparum*. The recombinant MSP-1(42) proteins are useful in diagnostic assays, for in vitro monitoring of malaria infection or prognosing the response to treatment of malaria patients, and for production of antibodies used for malaria antigen detection or as therapeutic or prophylactic agents

Sequence 391 AA:

Query Match 100.0%; Score 2071; DB 5; Length 391;

Best Local Similarity 100.0%; Pred. No. 1.7e-140;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAHHHHHPPGSGSGTMAISVTMDNISGFENEVDVYLKPLAGYRSLLKQIEKNITTF 60
DB 1 MAHHHHHPPGSGSGTMAISVTMDNISGFENEVDVYLKPLAGYRSLLKQIEKNITTF 60
QY 61 NLNLNDIINSRLKRRKYFLDVLSDLMQFKHISSENYIIEDSFKLNSEQNTLLKSYKY 120
DB 61 NLNLNDIINSRLKRRKYFLDVLSDLMQFKHISSENYIIEDSFKLNSEQNTLLKSYKY 120
QY 121 IKESVENDIKFAOGISYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDE 180
DB 121 IKESVENDIKFAOGISYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDE 180
QY 121 IKESVENDIKFAOGISYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDE 180
DB 121 IKESVENDIKFAOGISYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDE 180
QY 181 OKKESKFLPFLTNIETLYNNLVNKKIDYLLNLKAKINDCNVEKDEAHVKITKLSDLKAID 240
DB 181 OKKESKFLPFLTNIETLYNNLVNKKIDYLLNLKAKINDCNVEKDEAHVKITKLSDLKAID 240
QY 241 DKIDLFKNPYFEAIIKKLINDTKKDMGLKLSGLVONFPNTIISKLIIEGKFQDMLNIS 300
DB 241 DKIDLFKNPYFEAIIKKLINDTKKDMGLKLSGLVONFPNTIISKLIIEGKFQDMLNIS 300
QY 301 OHQCVKQCPENSGCFRHLDERECCCLNLYKQBGDKCVENPNPTCNENNGCCDADATCT 360
DB 301 OHQCVKQCPENSGCFRHLDERECCCLNLYKQBGDKCVENPNPTCNENNGCCDADATCT 360
QY 361 EEDGSSSRKKTTCCTKPDSPYLPFDGIFCSS 391
DB 361 EEDGSSSRKKTTCCTKPDSPYLPFDGIFCSS 391

```

RESULT 2

ID ABP71275 standard; protein; 391 AA.

AC ABP71275;

DT 28-APR-2003 (first entry)

XX E. coli expressed *P. falciparum* MSP1\_42 (3D7) protein sequence.

KW MSP-1\_42; merozoite protein; protozoacide; vaccine; malaria; mosquito.

XX Plasmodium *falciparum*.

OS WO2003004525-A2.

XX 16-JAN-2003.

XX 25-JAN-2002; 2002WO-US002428.

XX 29-JAN-2001; 2001US-0264535P.

XX 26-OCT-2001; 2001US-0347564P.

XX (REED-) REED ARMY INST RES WALTER.

XX Lyon JA, Angov E;

XX WPI; 2003-221577/21.

PT New recombinant Plasmodium *falciparum* merozoite protein (MSP)-142 which retains its native folding, useful for detecting and preventing malaria infection, and for antibody production.

PS Disclosure; Page 103; 104pp; English.

XX The invention relates to a recombinant Plasmodium *falciparum* merozoite protein, (MSP)-142 which retains its native folding. The protein is useful as a diagnostic reagent, in antibody production, and as a vaccine against malaria. The antibody may also be used for detecting and treating chronic malaria infection. The present sequence represents a recombinant E. coli expressed *P. falciparum* MAP-1\_42 protein

Sequence 391 AA:

Query Match 100.0%; Score 2071; DB 6; Length 391;

Best Local Similarity 100.0%; Pred. No. 1.7e-140;

Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAHHHHHPPGSGSGTMAISVTMDNISGFENEVDVYLKPLAGYRSLLKQIEKNITTF 60
DB 1 MAHHHHHPPGSGSGTMAISVTMDNISGFENEVDVYLKPLAGYRSLLKQIEKNITTF 60
QY 61 NLNLNDIINSRLKRRKYFLDVLSDLMQFKHISSENYIIEDSFKLNSEQNTLLKSYKY 120
DB 61 NLNLNDIINSRLKRRKYFLDVLSDLMQFKHISSENYIIEDSFKLNSEQNTLLKSYKY 120
QY 121 IKESVENDIKFAOGISYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDE 180
DB 121 IKESVENDIKFAOGISYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDE 180
QY 121 IKESVENDIKFAOGISYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDE 180
DB 121 IKESVENDIKFAOGISYYEKVLAKYKDDLESIKKVIKEEKEKFPSSPPTPPSPAKTDE 180
QY 181 OKKESKFLPFLTNIETLYNNLVNKKIDYLLNLKAKINDCNVEKDEAHVKITKLSDLKAID 240
DB 181 OKKESKFLPFLTNIETLYNNLVNKKIDYLLNLKAKINDCNVEKDEAHVKITKLSDLKAID 240
QY 241 DKIDLFKNPYFEAIIKKLINDTKKDMGLKLSGLVONFPNTIISKLIIEGKFQDMLNIS 300
DB 241 DKIDLFKNPYFEAIIKKLINDTKKDMGLKLSGLVONFPNTIISKLIIEGKFQDMLNIS 300
QY 301 OHQCVKQCPENSGCFRHLDERECCCLNLYKQBGDKCVENPNPTCNENNGCCDADATCT 360
DB 301 OHQCVKQCPENSGCFRHLDERECCCLNLYKQBGDKCVENPNPTCNENNGCCDADATCT 360
QY 361 EEDGSSSRKKTTCCTKPDSPYLPFDGIFCSS 391
DB 361 EEDGSSSRKKTTCCTKPDSPYLPFDGIFCSS 391

```

RESULT 3

ID ADM86524 standard; protein; 391 AA.

AC ADM86524;

DT 03-JUN-2004 (first entry)

XX E. coli expressed Plasmodium *falciparum* MSP142 (3D7) protein.

KW Malaria; vaccine; merozoite surface protein-142; MSP-142; immune response; diagnosis.

XX Plasmodium *falciparum*.

OS US2003161839-A1.

XX 28-AUG-2003.

XX 25-JAN-2002; 2002US-00057532.

XX 29-JAN-2001; 2001US-0264535P.



```
RESULT 5
ABP71273
ID ABP71273 standard; protein; 393 AA.
XX
AC ABP71273;
XX
DT 28-APR-2003 (first entry)
XX
DE P. falciparum MSP1_42 (3D7) protein sequence in clone pET42A.
XX
KW MSP-1_42; merozoite protein; protozoacide; vaccine; malaria; mosquito.
XX
OS Plasmodium falciparum.
XX
PN WO2003004525-A2.
XX
PD 16-JAN-2003.
XX
PF 25-JAN-2002; 2002WO-US002428.
XX
PR 29-JAN-2001; 2001US-0264535P.
PR 26-OCT-2001; 2001US-0347564P.
XX
PA (REED-) REED ARMY INST RES WALTER.
XX
PI Lyon JA, Angov E;
XX
DR WPI; 2003-221577/21.
XX
PT New recombinant Plasmodium falciparum merozoite protein (MSP)-142 which
PT retains its native folding, useful for detecting and preventing malaria
PT infection, and for antibody production.
XX
PS Disclosure; Page 96-97; 104pp; English.
XX
CC The invention relates to a recombinant Plasmodium falciparum merozoite
CC protein, (MSP)-142 which retains its native folding. The protein is
CC useful as a diagnostic reagent, in antibody production, and as a vaccine
CC against malaria. The antibody may also be used for detecting and treating
CC chronic malaria infection. The present sequence represents a recombinant
CC E. coli expressed P. falciparum MAP-1_42 protein expressed in clone
CC pET42A
XX
SQ Sequence 393 AA;
XX
Query Match 99.2%; Score 2055; DB 6; Length 393;
Best Local Similarity 99.2%; Pred. No. 2,4e-139;
Matches 390; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
1 MAHHHHHPGGS--GSGTMAISVTMDNIIISGFENEYDVIYIKPLAGVYRSIKKOIEKNIF 58
1 MAHHHHHPGGSIEGRGTMAISVTMDNIIISGFENEYDVIYIKPLAGVYRSIKKOIEKNIF 60
1 MAHHHHHPGGSIEGRGTMAISVTMDNIIISGFENEYDVIYIKPLAGVYRSIKKOIEKNIF 60
59 TFNLNDILNSRLKKRKYFLDVLES DLMQFKHSSNEYYIEDSFKLNSRQKXTLLKSY 118
61 TFNLNDILNSRLKKRKYFLDVLES DLMQFKHSSNEYYIEDSFKLNSRQKXTLLKSY 120
119 KYIKESVNDIKFAQEGISYIEKYLAKYKDDLESIKKVIKEKEKFPSSPTTPPSPAKT 178
121 KYIKESVNDIKFAQEGISYIEKYLAKYKDDLESIKKVIKEKEKFPSSPTTPPSPAKT 180
179 DEQKKESKFLPFLTNIETLTNNLVNKIDYILNKKAKINDCNVEKDBAHVKITKLSDLKA 238
181 DEQKKESKFLPFLTNIETLTNNLVNKIDYILNKKAKINDCNVEKDBAHVKITKLSDLKA 240
239 IDDKTIDLFKNPYDFEAIKKLINDTKDMLGKLTSGLVONFPNTIISKLEGGQDMLN 298
241 IDDKTIDLFKNPYDFEAIKKLINDTKDMLGKLTSGLVONFPNTIISKLEGGQDMLN 300
299 ISQHQCVCQCPENSGCFRHLDERECCCLNLYKQEGDKCVENPNPTCNENNGCDDADAT 358
```

```
DB 301 ISQHQCVCQCPENSGCFRHLDERECCCLNLYKQEGDKCVENPNPTCNENNGCDDADAT 360
OY 359 CTEEDSGSSRRKKTCECTKPDSPYPLFDGIFCSS 391
DB 361 CTEEDSGSSRRKKTCECTKPDSPYPLFDGIFCSS 393
RESULT 6
ADM86520
ID ADM86520 standard; protein; 393 AA.
XX
AC ADM86520;
XX
DT 03-JUN-2004 (first entry)
XX
DE pET42A Plasmodium falciparum MSP142 (3D7) protein.
XX
KW Malaria; vaccine; merozoite surface protein-142; MSP-142;
XX immune response; diagnosis.
XX
OS Plasmodium falciparum.
XX
PN US2003161839-A1.
XX
PD 28-AUG-2003.
XX
PF 25-JAN-2002; 2002US-00057532.
XX
PR 29-JAN-2001; 2001US-0264535P.
PR 26-OCT-2001; 2001US-0347563P.
XX
PA (LYON/) LYON J A.
PA (ANGOV/) ANGOV E.
PA (COHEN/) COHEN J D.
PA (VOSS/) VOSS G.
XX
PI Lyon JA, Angov E, Cohen JD, Voss G;
XX
DR WPI; 2003-843522/78.
XX
PT Malaria vaccine comprises Plasmodium falciparum merozoite surface protein
PT -142.
XX
PS Disclosure; SEQ ID NO 3; 41pp; English.
XX
CC The invention relates to a malaria vaccine which comprises Plasmodium
CC falciparum merozoite surface protein-142 (MSP-142) and an adjuvant
CC consisting of A, B, C, D, and E. The invention also relates to a method
CC for inducing protective immune response to malaria. The invention is used
CC as diagnostic reagent for antibody production or as vaccine against
CC malaria infection. The present sequence is Escherichia coli expressed P.
CC falciparum MSP142 (3D7) protein sequence in pET42A. This sequence is used
CC to illustrate the method of the invention.
XX
SQ Sequence 393 AA;
XX
Query Match 99.2%; Score 2055; DB 7; Length 393;
Best Local Similarity 99.2%; Pred. No. 2,4e-139;
Matches 390; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
1 MAHHHHHPGGS--GSGTMAISVTMDNIIISGFENEYDVIYIKPLAGVYRSIKKOIEKNIF 58
1 MAHHHHHPGGSIEGRGTMAISVTMDNIIISGFENEYDVIYIKPLAGVYRSIKKOIEKNIF 60
59 TFNLNDILNSRLKKRKYFLDVLES DLMQFKHSSNEYYIEDSFKLNSRQKXTLLKSY 118
61 TFNLNDILNSRLKKRKYFLDVLES DLMQFKHSSNEYYIEDSFKLNSRQKXTLLKSY 120
119 KYIKESVNDIKFAQEGISYIEKYLAKYKDDLESIKKVIKEKEKFPSSPTTPPSPAKT 178
121 KYIKESVNDIKFAQEGISYIEKYLAKYKDDLESIKKVIKEKEKFPSSPTTPPSPAKT 180
179 DEQKKESKFLPFLTNIETLTNNLVNKIDYILNKKAKINDCNVEKDBAHVKITKLSDLKA 238
```

|||||  
Db DEQKESKFLPFLTNIETLYNNLVNKIDYLIINLAKKINDCIVEKDEAHVKITKLSDLKA 240  
Qy 239 IDDKIDLEFKNPYDFEAIKKLINDDTKDKMLGKGLSTGLVQNPFTNTIISKLEIGKQDMLN 298  
Db 241 IDDKIDLEFKNPYDFEAIKKLINDDTKDKMLGKGLSTGLVQNPFTNTIISKLEIGKQDMLN 300  
Qy 299 ISQHCVKQCCPENSGCFRHLDERBECKCLINYKQEGDKCVENPPTCNENNGCCDADAT 358  
Db 301 ISQHCVKQCCPENSGCFRHLDERBECKCLINYKQEGDKCVENPPTCNENNGCCDADAT 360  
Qy 359 CTBEDSGSSRRKKTICECTKPDSPYPLFDGIFCSS 391  
Db 361 CTBEDSGSSRRKKTICECTKPDSPYPLFDGIFCSS 393  
RESULT 7  
ID ABB79624 standard; protein; 431 AA.  
AC ABB79624;  
DT 21-OCT-2002 (first entry)  
DE E. coli expressed P. falciparum MSP-1 recombinant protein.  
KW Merozoite surface protein-1; MSP-1; malaria; vaccine; protozoacide.  
XX Plasmodium falciparum.  
OS Synthetic.  
OS Chimeric.  
XX MO200258727-A2.  
XX 01-AUG-2002.  
PD 25-JAN-2002; 2002WO-US002554.  
PF 26-JAN-2001; 2001US-0264535P.  
PR (REED-) REED ARMY INST RES WALTER.  
XX PA Lyon JA, Angov E, Cohen JD, Voss G;  
XX PI WPI; 2002-590798/63.  
DR  
XX PT New vaccine comprising Plasmodium falciparum MSP-142 protein and an  
PT adjuvant, useful against malaria or for eliciting immune responses  
PT against P. falciparum.  
XX PS  
PS Disclosure; Page 90-91; 99pp; English.  
XX  
CC The present sequence is that of a recombinant protein comprising  
CC Plasmodium falciparum 3D7 merozoite surface protein-1 42 kDa fragment  
CC (MSP-1(42)) with an N-terminal (His)6-tag for affinity purification and  
CC an additional vector-encoded sequence (approximately 50 amino acids)  
CC which include an enterokinase cleavage site, a S-peptide tag and a  
CC thrombin cleavage site fused to the N-terminus of MSP-1(42). The levels  
CC of expression of this fusion protein, encoded by plasmid pET(50)MSP-142,  
CC were 5-10% of total E. coli protein in crude cell lysates, and the  
CC protein was purified to near homogeneity with 2 consecutive passes over a  
CC Ni2+-NTA agarose resin. The present invention relates to the production  
CC of large amounts of MSP-1(42) which maintain conformational epitopes  
CC critical for development as vaccines. The vaccines are useful against  
CC malaria or for eliciting immune responses against P. falciparum. The  
CC recombinant MSP-1(42) proteins are useful in diagnostic assays, for in  
CC vitro monitoring of malaria infection or prognosing the response to  
CC treatment of malaria patients, and for production of antibodies used for  
CC malaria antigen detection or as therapeutic or prophylactic agents  
XX  
XX Sequence 431 AA;  
Query Match 97.0%; Score 2008.5; DB 5; Length 431;

Best Local Similarity 89.5%; Pred. No. 6e-136;  
Matches 385; Conservative 0; Mismatches 4; Indels 41; Gaps 1;  
Qy 3 HHHHHHPG-----SSGSMATSV 21  
Db 2 HHHHHSSGLVPRGSMKETAAAFERQHMDSPDIGTDDDKAMADISIGRGMAISV 61  
Qy 22 TMDNIIISGFENEYDVITYLKPLAGVYRSLSKKOIEKNIPTFNINLNDILNSRLKKRYFLDV 81  
Db 62 TMDNIIISGFENEYDVITYLKPLAGVYRSLSKKOIEKNIPTFNINLNDILNSRLKKRYFLDV 121  
Qy 82 LESDLMQFKHIISSNEYIIEDSPKLIINSQKNTLLKSYRYIESYVNDIKFAQEGISYSEK 141  
Db 122 LESDLMQFKHIISSNEYIIEDSPKLIINSQKNTLLKSYRYIESYVNDIKFAQEGISYSEK 181  
Qy 142 VLAKYKDDLESIIKKYIKSEKKEKFPSSPTTPSPAKTDEQKESKFLPFLTNIETLYNNL 201  
Db 182 VLAKYKDDLESIIKKYIKSEKKEKFPSSPTTPSPAKTDEQKESKFLPFLTNIETLYNNL 241  
Qy 202 VNKIDYLIINLAKKINDCIVEKDEAHVKITKLSDLKAIDDKIDLEFKNPYDFEAIKKLIND 261  
Db 242 VNKIDYLIINLAKKINDCIVEKDEAHVKITKLSDLKAIDDKIDLEFKNPYDFEAIKKLIND 301  
Qy 262 DTKDKMLGKGLSTGLVQNPFTNTIISKLEIGKQDMLNISQHCVKQCCPENSGCFRHLDE 321  
Db 302 DTKDKMLGKGLSTGLVQNPFTNTIISKLEIGKQDMLNISQHCVKQCCPENSGCFRHLDE 361  
Qy 322 REECKCLINYKQEGDKCVENPPTCNENNGCCDADATCTBEDSGSSRRKKTICECTKPDSPY 381  
Db 362 REECKCLINYKQEGDKCVENPPTCNENNGCCDADATCTBEDSGSSRRKKTICECTKPDSPY 421  
Qy 382 PLFDGIFCSS 391  
Db 422 PLFDGIFCSS 431  
RESULT 8  
ID ABB71272 standard; protein; 431 AA.  
AC ABB71272;  
DT 28-APR-2003 (first entry)  
DE P. falciparum MSP1\_42 (3D7) protein sequence in clone pET(50)MSP1-42.  
XX KW MSP-1\_42; merozoite protein; protozoacide; vaccine; malaria; mosquito.  
XX OS Plasmodium falciparum.  
XX PN WO2003004525-A2.  
XX  
XX 16-JAN-2003.  
PD 25-JAN-2002; 2002WO-US002428.  
PF 29-JAN-2001; 2001US-0264535P.  
PR 26-OCT-2001; 2001US-0347364P.  
XX PA (REED-) REED ARMY INST RES WALTER.  
XX PI Lyon JA, Angov E;  
XX WPI; 2003-221577/21.  
DR  
XX  
XX New recombinant Plasmodium falciparum merozoite protein (MSP)-142 which  
XX PT retains its native folding, useful for detecting and preventing malaria  
XX PT infection, and for antibody production.  
XX  
XX Claim 5; Page 95-96; 104pp; English.  
XX  
XX The invention relates to a recombinant Plasmodium falciparum merozoite  
XX CC protein, (MSP)-1\_42 which retains its native folding. The protein is

CC useful as a diagnostic reagent, in antibody production, and as a vaccine  
 CC against malaria. The antibody may also be used for detecting and treating  
 CC chronic malaria infection. The present sequence represents a recombinant  
 CC E. coli expressed P. falciparum MAP-1\_42 protein expressed in clone  
 CC per(50)MSP1-42

XX Sequence 431 AA;

Query Match 97.0%; Score 2008.5; DB 6; Length 431;  
 Best Local Similarity 89.5%; Pred. No. 6e-136;  
 Matches 385; Conservative 0; Mismatches 4; Indels 41; Gaps 1;

QY 3 HHHHHHPGG-----SSGSTMATSV 21  
 DB 2 HHHHHSSGLVPRGSGMKETAAPFEROHMSPDLGTDHDDKAMADIGSIEGRGTMAISV 61  
 QY 22 TMDNITLSGFENEYDIYIKPLAGVYRSLSKKQIEKNIFPNLNLNDILNSRLKKRYFLDV 81  
 DB 62 TMDNITLSGFENEYDIYIKPLAGVYRSLSKKQIEKNIFPNLNLNDILNSRLKKRYFLDV 121  
 QY 82 LESDLMQFKHISNNEYIIEDSFKLNSBOKNTLSKYKIKESVENDIKFAQEGISYEEK 141  
 DB 122 LESDLMQFKHISNNEYIIEDSFKLNSBOKNTLSKYKIKESVENDIKFAQEGISYEEK 181  
 QY 142 VLAKYKODLESIKKVIKEKEKEFPSSPTTPPSPAKTDEQKESKFLPFLTNIEFLYNNL 201  
 DB 182 VLAKYKODLESIKKVIKEKEKEFPSSPTTPPSPAKTDEQKESKFLPFLTNIEFLYNNL 241  
 QY 202 VNKIDDYILINLKAKINDCNVEKDEAHVKTLSDLKATDDKIDLPKNPYDEFAIKKLIND 261  
 DB 242 VNKIDDYILINLKAKINDCNVEKDEAHVKTLSDLKATDDKIDLPKNPYDEFAIKKLIND 301  
 QY 262 DTKDMGLKSLSTGLVQNFPTTIISKLEGFQDMLNISQHCYKQCPENSGCFRHLDE 321  
 DB 302 DTKDMGLKSLSTGLVQNFPTTIISKLEGFQDMLNISQHCYKQCPENSGCFRHLDE 361  
 QY 322 REECKCLLNKYQEGDKCVENPNPTCNENNGCGDADATCTEEDSGSSRRKKTCECTKPSY 381  
 DB 362 REECKCLLNKYQEGDKCVENPNPTCNENNGCGDADATCTEEDSGSSRRKKTCECTKPSY 421  
 QY 382 PLFDGIFCSS 391  
 DB 422 PLFDGIFCSS 431

#### RESULT 9

ADM86519 ID ADM86519 standard; protein; 431 AA.

XX ADM86519;  
 AC  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE per(50)MSP1-42 P. falciparum MSP142 (3D7) protein.  
 XX  
 KW Malaria; vaccine; merozoite surface protein-142; MSP-142;  
 KW immune response; diagnosis.  
 XX  
 OS Plasmodium falciparum.  
 XX  
 PN US2003161839-A1.  
 PD  
 XX 28-AUG-2003.  
 PE 25-JAN-2002; 2002US-00057532.  
 XX  
 PR 29-JAN-2001; 2001US-0264535P.  
 PR 26-OCT-2001; 2001US-0347563P.  
 XX  
 PA (LYON/) LYON J A.  
 PA (ANGOV/) ANGOV E.  
 PA (COHEN/) COHEN J D.  
 PA (VOSS/) VOSS G.

XX Lyon JA, Angov E, Cohen JD, Voss G;  
 XX WPI; 2003-843522/78.

PT Malaria vaccine comprises Plasmodium falciparum merozoite surface protein  
 PT -142.  
 PS Disclosure; SEQ ID NO 2; 41pp; English.

CC The invention relates to a malaria vaccine which comprises Plasmodium  
 CC falciparum merozoite surface protein-142 (MSP-142), and an adjuvant  
 CC consisting of A, B, C, D, and E. The invention also relates to a method  
 CC for inducing protective immune response to malaria. The invention is used  
 CC as diagnostic reagent for antibody production or as vaccine against  
 CC malaria infection. The present sequence is Escherichia coli expressed P.  
 CC falciparum MSP142 (3D7) protein sequence in per(50)MSP1-42. This sequence  
 CC is used to illustrate the method of the invention.

XX Sequence 431 AA;

Query Match 97.0%; Score 2008.5; DB 7; Length 431;  
 Best Local Similarity 89.5%; Pred. No. 6e-136;  
 Matches 385; Conservative 0; Mismatches 4; Indels 41; Gaps 1;

QY 3 HHHHHHPGG-----SSGSTMATSV 21  
 DB 2 HHHHHSSGLVPRGSGMKETAAPFEROHMSPDLGTDHDDKAMADIGSIEGRGTMAISV 61  
 QY 22 TMDNITLSGFENEYDIYIKPLAGVYRSLSKKQIEKNIFPNLNLNDILNSRLKKRYFLDV 81  
 DB 62 TMDNITLSGFENEYDIYIKPLAGVYRSLSKKQIEKNIFPNLNLNDILNSRLKKRYFLDV 121  
 QY 82 LESDLMQFKHISNNEYIIEDSFKLNSBOKNTLSKYKIKESVENDIKFAQEGISYEEK 141  
 DB 122 LESDLMQFKHISNNEYIIEDSFKLNSBOKNTLSKYKIKESVENDIKFAQEGISYEEK 181  
 QY 142 VLAKYKODLESIKKVIKEKEKEFPSSPTTPPSPAKTDEQKESKFLPFLTNIEFLYNNL 201  
 DB 182 VLAKYKODLESIKKVIKEKEKEFPSSPTTPPSPAKTDEQKESKFLPFLTNIEFLYNNL 241  
 QY 202 VNKIDDYILINLKAKINDCNVEKDEAHVKTLSDLKATDDKIDLPKNPYDEFAIKKLIND 261  
 DB 242 VNKIDDYILINLKAKINDCNVEKDEAHVKTLSDLKATDDKIDLPKNPYDEFAIKKLIND 301  
 QY 262 DTKDMGLKSLSTGLVQNFPTTIISKLEGFQDMLNISQHCYKQCPENSGCFRHLDE 321  
 DB 302 DTKDMGLKSLSTGLVQNFPTTIISKLEGFQDMLNISQHCYKQCPENSGCFRHLDE 361  
 QY 322 REECKCLLNKYQEGDKCVENPNPTCNENNGCGDADATCTEEDSGSSRRKKTCECTKPSY 381  
 DB 362 REECKCLLNKYQEGDKCVENPNPTCNENNGCGDADATCTEEDSGSSRRKKTCECTKPSY 421  
 QY 382 PLFDGIFCSS 391  
 DB 422 PLFDGIFCSS 431

#### RESULT 10

ABB79623 ID ABB79623 standard; protein; 546 AA.

XX ABB79623;  
 AC  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE E. coli expressed P. falciparum MSP-1 recombinant protein.  
 XX  
 KW Merozoite surface protein-1; MSP-1; chloroquine; malaria; vaccine;  
 KW protozoicide.  
 XX  
 OS Plasmodium falciparum.



[illegible]

QY	322	REBCKCLNLYKQEGKVCVENPPTCNENNGGCDADATCTEEDSGSSRKXITCECTKPPSY	381
DB	477	REBCKCLNLYKQEGKVCVENPPTCNENNGGCDADATCTEEDSGSSRKXITCECTKPPSY	536
QY	382	PLFDGIFCSS 391	
DB	537	PLFDGIFCSS 546	
RESULT 11			
ABP71271	ABP71271	standard; protein; 546 AA.	
AC	ABP71271;		
DT	28-APR-2003	(first entry)	
DE	P. falciparum MSP1_42 (3D7)	protein sequence in clone per-Trx42.	
XX	MSP-1_42; merozoite protein; protozoacide; vaccine; malaria; mosquito.		
XX	Plasmodium falciparum.		
XX	MO200304525-A2.		
PD	16-JAN-2003.		
XX	25-JAN-2002; 2002WO-US002428.		
XX	29-JAN-2001; 2001US-0264535P.		
PR	26-OCT-2001; 2001US-0347564P.		
XX	(REED-) REED ARMY INST RES WALTER.		
PI	Lyon JA, Angov E;		
XX	WPI; 2003-221577/21.		
DR			
PT	New recombinant Plasmodium falciparum merozoite protein (MSP)-142 which		
PT	retains its native folding, useful for detecting and preventing malaria		
PT	infection, and for antibody production.		
XX	Disclosure; Page 93-95; 104pp; English.		
XX	The invention relates to a recombinant Plasmodium falciparum merozoite		
CC	protein, (MSP)-142 which retains its native folding. The protein is		
CC	useful as a diagnostic reagent, in antibody production, and as a vaccine		
CC	against malaria. The antibody may be used for detecting and treating		
CC	chronic malaria infection. The present sequence represents a recombinant		
CC	E. coli expressed P. falciparum MAP-1_42 protein expressed in clone per-		
CC	Trx42		
XX			
XX	Sequence 546 AA:		
QY	Query Match	97.0%; Score 2008.5; DB 6; Length 546;	
DB	Best Local Similarity	89.5%; Pred. No. 8.3e-136;	
	Matches 385; Conservative	0; Mismatches 4; Indels 41; Gaps 1;	
QY	3 HHHHHHGG-----SGSGTMAISV 21		
DB	117 HHHHHHSSGLVPRGSGMKETAAKFEROHMDSPLGTDHDDKAMADIGSIEGRGTMAISV 176		
QY	22 TMDNIIISGFENEYDVIIYKPLAGVYRSLLKQIEKNIFTFNINLNDILNSRLKKRYFLDV 81		
DB	177 TMDNIIISGFENEYDVIIYKPLAGVYRSLLKQIEKNIFTFNINLNDILNSRLKKRYFLDV 236		
QY	82 LESDLMQFKHISNNEYIIEDSFKLINSEQNTLLSKYKIKESYVENDIKFAQEGISYIEK 141		
DB	237 LESDLMQFKHISNNEYIIEDSFKLINSEQNTLLSKYKIKESYVENDIKFAQEGISYIEK 296		
QY	142 VLATYKQDLESIKKVIIEEKEKEFPSSSPPTTPSPAKTDEQKESKPLPFLNIETLVNVL 201		
DB	297 VLATYKQDLESIKKVIIEEKEKEFPSSSPPTTPSPAKTDEQKESKPLPFLNIETLVNVL 356		

QY 202 VNKIDYVILNKAKINDCNVEKDEAHVKTITKLSDKAIDDKIDLFPKNPYDFAIKKLIND 261  
 DB 357 VNKIDYVILNKAKINDCNVEKDEAHVKTITKLSDKAIDDKIDLFPKNPYDFAIKKLIND 416  
 QY 262 DTKDMLGKLTSTGLVQNFPTTIIISKLIEGKFQDMLNISQHCYVKQCPENSGCFRHLDE 321  
 DB 417 DTKDMLGKLTSTGLVQNFPTTIIISKLIEGKFQDMLNISQHCYVKQCPENSGCFRHLDE 476  
 QY 322 REECCLLNKYQEGDKCVENPPTCNENNGGCDADATCTEEDSGSSRRKKTCECTKPPSY 381  
 DB 477 REECCLLNKYQEGDKCVENPPTCNENNGGCDADATCTEEDSGSSRRKKTCECTKPPSY 536  
 QY 382 PLFDGIFCSS 391  
 DB 537 PLFDGIFCSS 546

RESULT 12  
 ADM86518  
 ID ADM86518 standard; protein; 546 AA.

XX AC ADM86518;  
 XX DT 03-JUN-2004 (first entry)  
 XX DE PEF-Trx42 P. falciparum MSP142 (3D7) protein.  
 XX KW Malaria / vaccine / merozoite surface protein-142 ; MSP-142 ;  
 KW immune response; diagnosis.  
 XX OS Plasmodium falciparum.  
 XX PN US2003161839-A1.  
 XX PD 28-AUG-2003.  
 XX PF 25-JAN-2002; 2002US-00057532.  
 XX PR 29-JAN-2001; 2001US-0264535P.  
 XX PR 26-OCT-2001; 2001US-0347563P.  
 XX PA (LYON/) LYON J A.  
 XX PA (ANGO/) ANGOV E.  
 XX PA (COHE/) COHEN J D.  
 XX PA (VOSS/) VOSS G.  
 XX PI Lyon JA, Angov E, Cohen JD, Voss G;  
 XX DR WPI; 2003-843522/78.  
 XX PS Malaria vaccine comprises Plasmodium falciparum merozoite surface protein  
 PT -142.  
 XX PS Malaria vaccine comprises Plasmodium falciparum merozoite surface protein  
 XX PS Disclouseure; SEQ ID NO 1; 41pp; English.  
 CC CC The invention relates to a malaria vaccine which comprises plasmodium  
 CC falciparum merozoite surface protein-142 (MSP-142) , and an adjuvant  
 CC consisting of A, B, C, D, and E. The invention also relates to a method  
 CC for inducing protective immune response to malaria. The invention is used  
 CC as diagnostic reagent for antibody production or as vaccine against  
 CC malaria infection. The present sequence is Escherichia coli expressed P.  
 CC falciparum MSP142 (3D7) protein sequence in PEF-Trx42. This sequence is  
 CC used to illustrate the method of the invention.  
 XX SQ Sequence 546 AA;

Query Match 97.0%; Score 2008.5; DB 7; Length 546;  
 Best Local Similarity 89.5%; Pred. No. 8.3e-136;  
 Matches 385; Conservative 0; Mismatches 4; Indels 41; Gaps 1;  
 QY 3 HHHHHHPCG-----SSGSTMALSV 21  
 ||||| |  
 |

DB 117 HHHHHSSGLVPRGSMKETAARFERQHMDS PDLGTDDDKAMADIGSIEGRGTMAISV 176  
 QY 22 TMDNLSGFENEVDYIYKPLAGVYRS,KQIEKNITFTFNILNDILNSRLKRYFLDV 81  
 DB 177 TMDNLSGFENEVDYIYKPLAGVYRS,KQIEKNITFTFNILNDILNSRLKRYFLDV 236  
 QY 82 LESDLMQFKHISSENEYIIESDFKLNSQKNTLLKSYRIKESVENDIKFAOEGISYEEK 141  
 DB 227 LESDLMQFKHISSENEYIIESDFKLNSQKNTLLKSYRIKESVENDIKFAOEGISYEEK 296  
 QY 142 VLAKKQDLSEIKKRIKEKEKFPSSPTTTPSPAKTDEQKESKFLPLFNIEFLVNL 201  
 DB 297 VLAKKQDLSEIKKRIKEKEKFPSSPTTTPSPAKTDEQKESKFLPLFNIEFLVNL 356  
 QY 202 VNKIDYVILNKAKINDCNVEKDEAHVKTITKLSDKAIDDKIDLFPKNPYDFAIKKLIND 261  
 DB 357 VNKIDYVILNKAKINDCNVEKDEAHVKTITKLSDKAIDDKIDLFPKNPYDFAIKKLIND 416  
 QY 262 DTKDMLGKLTSTGLVQNFPTTIIISKLIEGKFQDMLNISQHCYVKQCPENSGCFRHLDE 321  
 DB 417 DTKDMLGKLTSTGLVQNFPTTIIISKLIEGKFQDMLNISQHCYVKQCPENSGCFRHLDE 476  
 QY 322 REECCLLNKYQEGDKCVENPPTCNENNGGCDADATCTEEDSGSSRRKKTCECTKPPSY 381  
 DB 477 REECCLLNKYQEGDKCVENPPTCNENNGGCDADATCTEEDSGSSRRKKTCECTKPPSY 536  
 QY 382 PLFDGIFCSS 391  
 DB 537 PLFDGIFCSS 546

RESULT 13  
 AAB83926  
 ID AAB83926 standard; protein; 375 AA.

XX AC AAB83926;  
 XX DT 23-JUL-2001 (first entry)  
 XX DE A major merozoite surface protein-1 fragment of 42kDa.  
 XX KW Major merozoite surface protein-1; MSP1-42; melittin signal peptide;  
 KW malaria vaccine.  
 XX OS Plasmodium falciparum.  
 XX PN WO200134188-A1.  
 XX PD 17-MAY-2001.  
 XX PF 09-NOV-2000; 2000WO-US031064.  
 XX PR 12-NOV-1999; 98US-0165178P.  
 XX PR 01-DEC-1999; 98US-0168327P.  
 XX PR 22-AUG-2000; 2000US-0226861P.  
 XX PA (UYHA-) UNIV HAWAII.  
 XX PA (UYCH-) UNIV CHINESE HONG KONG.  
 XX PA (QUEB-) QUEBEN EMMA FOUND.  
 XX PI Hui GSN, Lap-Yin P, Ho WKK;  
 XX DR WPI; 2001-335879/35.  
 XX DR N-P8DB; AAF89840.

Producing malaria vaccine, useful for treatment or prevention of all  
 PT forms of malaria in humans, by expressing immunogenic merozoite protein  
 PT fragment in a baculovirus system.  
 XX Example 3; Page 87-88; 95pp; English.  
 CC The present sequence represents a major merozoite surface protein-1 C-  
 CC terminal fragment of 42kDa (MSP1-42). This fragment is linked to a

CC melittin signal peptide, and then expressed in a in a  
CC silkworm/baculovirus system. The protein is used to prepare a malaria  
CC vaccine, which is used to treat or prevent malaria, caused by any of the  
CC four species of Plasmodium that infect humans

XX Sequence 375 AA;

Query Match 95.1%; Score 1970; DB 4; Length 375;  
Best Local Similarity 100.0%; Pred. No. 3e-133;  
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 17 MAISTYMDNIISGFENEYDVYILKPLAGVYRSLLKKQIEKNITFTNLNDILNSRLKRX 76
DB 1 MAISTYMDNIISGFENEYDVYILKPLAGVYRSLLKKQIEKNITFTNLNDILNSRLKRX 60
QY YFLDVLSESDLMQFHIISSNEYIIEDSFKLNSQKNTLLKSYKIKESVENDIKFAQEG 136
DB YFLDVLSESDLMQFHIISSNEYIIEDSFKLNSQKNTLLKSYKIKESVENDIKFAQEG 120
QY 1137 SYEKVLAKYKDDLESIKKVIEKEKEKFPSSPPTTPSPAKTDQKESKFLPLTNIET 196
DB 121 SYEKVLAKYKDDLESIKKVIEKEKEKFPSSPPTTPSPAKTDQKESKFLPLTNIET 180
QY 197 LYNNLVNKKIDYILNLKAKINDCNVEKDBAHVKTITKLSDLKAIIDKIDLFKNPYDEAIK 256
DB 181 LYNNLVNKKIDYILNLKAKINDCNVEKDBAHVKTITKLSDLKAIIDKIDLFKNPYDEAIK 240
QY 257 KLINDPTKKDMLGKLSTGLVQNFNTIISKLEBGFQDMLNISQHCVKKQCPENSGCF 316
DB 241 KLINDPTKKDMLGKLSTGLVQNFNTIISKLEBGFQDMLNISQHCVKKQCPENSGCF 300
QY 317 RHLDERECKCLANVKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECT 376
DB 301 RHLDERECKCLANVKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKITCECT 360
QY 377 KPDSYPLFDGIFGSS 391
DB 361 KPDSYPLFDGIFGSS 375
```

RESULT 14  
ABB79626  
ID ABB79626 standard; protein; 383 AA.  
XX  
AC ABB79626;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Plasmodium falciparum merozoite surface protein-1 42 kDa fragment.  
XX  
KW Merozoite surface protein-1; MSP-1; malaria; vaccine; protozoacide.  
XX  
OS Plasmodium falciparum.  
XX  
PN W0200258727-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 25-JAN-2002; 2002WO-US002554.  
XX  
PR 26-JAN-2001; 2001US-0264535P.  
XX  
PA (REED-) REED ARMY INST RES WALTER.  
XX  
PI Lyon JA, Angov E, Cohen JD, Voss G;  
XX  
DR WPI; 2002-590798/63.  
XX  
PT New vaccine comprising Plasmodium falciparum MSP-142 protein and an  
PT adjuvant, useful against malaria or for eliciting immune responses  
PT against P. falciparum.  
XX  
PS Disclosure; Page 95-96; 9pp; English.

XX The present sequence is the protein sequence of the C-terminal 42 kDa  
CC fragment of Plasmodium falciparum 3D7 merozoite surface protein-1 (MSP-  
CC 1(42)). The invention relates to the use of Escherichia coli as host for  
CC the recombinant production of large amounts of MSP-1(42) which maintain  
CC conformational epitopes critical for development of vaccines. The  
CC vaccines are useful against malaria or for eliciting immune responses  
CC against P. falciparum. The recombinant MSP-1(42) proteins are also useful  
CC in diagnostic assays, for in vitro monitoring of malaria infection or  
CC prognosis the response to treatment of malaria patients, and for  
CC production of antibodies used for malaria antigen detection or as  
CC therapeutic or prophylactic agents

XX Sequence 383 AA;

Query Match 95.0%; Score 1968; DB 5; Length 383;  
Best Local Similarity 99.2%; Pred. No. 4.3e-133;  
Matches 376; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 13 GSGTMAISVTMDNIIISGFENEYDVYILKPLAGVYRSLLKKQIEKNITFTNLNDILNSRL 72
DB 5 GSGTMAISVTMDNIIISGFENEYDVYILKPLAGVYRSLLKKQIEKNITFTNLNDILNSRL 64
QY 73 KRRKYFLDVLSESDLMQFHIISSNEYIIEDSFKLNSQKNTLLKSYKIKESVENDIKFA 132
DB 65 KRRKYFLDVLSESDLMQFHIISSNEYIIEDSFKLNSQKNTLLKSYKIKESVENDIKFA 124
QY 133 QEGISYEVKVLAKYKDDLESIKKVIEKEKEKFPSSPPTTPSPAKTDQKESKFLPLT 192
DB 125 QEGISYEVKVLAKYKDDLESIKKVIEKEKEKFPSSPPTTPSPAKTDQKESKFLPLT 184
QY 193 NIETLYNNLVNKKIDYILNLKAKINDCNVEKDBAHVKTITKLSDLKAIIDKIDLFKNPYDE 252
DB 185 NIETLYNNLVNKKIDYILNLKAKINDCNVEKDBAHVKTITKLSDLKAIIDKIDLFKNPYDE 244
QY 253 EAIKKLINDPTKKDMLGKLSTGLVQNFNTIISKLEBGFQDMLNISQHCVKKQCPEN 312
DB 245 EAIKKLINDPTKKDMLGKLSTGLVQNFNTIISKLEBGFQDMLNISQHCVKKQCPEN 304
QY 313 SGCPRHLDERECKCLANVKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKIT 372
DB 305 SGCPRHLDERECKCLANVKQEGDKCVENPNPTCNENNGGCDADATCTEEDSGSSRKKIT 364
QY 373 CECTKPDSYPLFDGIFGSS 391
DB 365 CECTKPDSYPLFDGIFGSS 383
```

RESULT 15  
ABP71274  
ID ABP71274 standard; protein; 383 AA.  
XX  
AC ABP71274;  
XX  
DT 28-APR-2003 (first entry)  
XX  
DE P. falciparum MSP\_142 protein sequence in pMBP.  
XX  
KW MSP-1\_42; merozoite protein; protozoacide; vaccine; malaria; mosquito.  
XX  
OS Plasmodium falciparum.  
XX  
PN W02003004525-A2.  
XX  
PD 16-JAN-2003.  
XX  
PF 25-JAN-2002; 2002WO-US002428.  
XX  
PR 29-JAN-2001; 2001US-0264535P.  
PR 26-OCT-2001; 2001US-0347564P.  
XX  
PA (REED-) REED ARMY INST RES WALTER.  
XX

PI Lyon JA, Angov E;  
XX  
XX WPI: 2003-221577/21.

DR  
XX  
PT New recombinant Plasmodium falciparum merozoite protein (MSP)-142 which  
PT retains its native folding, useful for detecting and preventing malaria  
PT infection, and for antibody production.

XX  
PS Disclosure; Page 99-100; 104pp; English.

CC The invention relates to a recombinant Plasmodium falciparum merozoite  
CC protein, (MSP)-142 which retains its native folding. The protein is  
CC useful as a diagnostic reagent, in antibody production, and as a vaccine  
CC against malaria. The antibody may also be used for detecting and treating  
CC chronic malaria infection. The present sequence represents a recombinant  
CC E. coli expressed P. falciparum MAP-1\_42 protein expressed in pMBP

XX  
SQ Sequence 383 AA;

Query Match 95.0%; Score 1968; DB 6; Length 383;

Best Local Similarity 99.2%; Pred. No. 4,3e-133; Indels 0; Gaps 0;

Matches 376; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	13	GGGTAAISVTMDNLTSGFENEYDVIYLPKAGVRSLLKKQIEKNIFTFNLINDILNSRL	72
DB	5	GRGTAAISVTMDNLTSGFENEYDVIYLPKAGVRSLLKKQIEKNIFTFNLINDILNSRL	64
QY	73	KKRKYFLDVLSDDLMOFGHISNEYIIEDSPFLNSBOKNTLKSXYIKESVENDIKFA	132
DB	65	KKRKYFLDVLSDDLMOFGHISNEYIIEDSPFLNSBOKNTLKSXYIKESVENDIKFA	124
QY	133	QEGISYVEKVLAKYKDDLESIKKVYKEEKEKFPSSPTTPSPAKTDEOKKESKFLPLT	192
DB	125	QEGISYVEKVLAKYKDDLESIKKVYKEEKEKFPSSPTTPSPAKTDEOKKESKFLPLT	184
QY	193	NIETLYNNLVNKKIDDYLLNLKAKINDCNVEKDEAHVKITKLSDLKAIIDDKIDLFQNPYDF	252
DB	185	NIETLYNNLVNKKIDDYLLNLKAKINDCNVEKDEAHVKITKLSDLKAIIDDKIDLFQNPYDF	244
QY	253	EAIRKLINDDTKKDMLGKLLSTGLVQNPNTTISKILIEGKPODMLNISQHCVCVKQCPEN	312
DB	245	EAIRKLINDDTKKDMLGKLLSTGLVQNPNTTISKILIEGKPODMLNISQHCVCVKQCPEN	304
QY	313	SGCFPHLDREBECKCLLVYKQEGDKCVENPNPTCNENNCGCDADATCTEEDSGSSRKKIT	372
DB	305	SGCFPHLDREBECKCLLVYKQEGDKCVENPNPTCNENNCGCDADATCTEEDSGSSRKKIT	364
QY	373	CECTKPDSDYPLFDGIFCSS	391
DB	365	CECTKPDSDYPLFDGIFCSS	383

Search completed: May 5, 2006, 00:20:35  
Job time : 189 secs

Pricer avt

CURRENT FILING DATE: 2002-01-25  
 PRIOR APPLICATION NUMBER: US 60/264,535  
 PRIOR FILING DATE: 2001-01-26  
 PRIOR APPLICATION NUMBER: US 60/347,564  
 PRIOR FILING DATE: 2001-10-26  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: Apple Macintosh Microsoft Word 6.0  
 SEQ ID NO 1  
 LENGTH: 546  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE:  
 OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein  
 Patent No. 6855322  
 US-10-057-531A-1

Query Match  
 Best Local Similarity 97.0%; Score 2008.5; DB 2; Length 546;  
 Matches 385; Conservative 0; Mismatches 4; Indels 41; Gaps 1;

QY	3	HHHHHGGG	-----SGSGTMAISV 21
DB	117	HHHHHSSGLVPRGSGMKETAAAFERQHNDSPDLGTDDDKAMADIGSIEGRGTMAISV 176	
QY	22	TMDNITSGFENEYDVYIKPLAGYRSLSKQIEKNITFTFNINDILNSRLKRRKYFLDY 81	
DB	177	TMDNITSGFENEYDVYIKPLAGYRSLSKQIEKNITFTFNINDILNSRLKRRKYFLDY 81	
QY	82	LESDDLMOFGHISSENYIIEISFRLNSSEKNTLSKYKIKESVENDIKFAOGISYERK 141	
DB	237	LESDDLMOFGHISSENYIIEISFRLNSSEKNTLSKYKIKESVENDIKFAOGISYERK 141	
QY	142	VLAQRKDLESIKYIKERKEKFPSSPTTPSPAKTDEOKKESKFLPLTNIEETLNNL 201	
DB	297	VLAQRKDLESIKYIKERKEKFPSSPTTPSPAKTDEOKKESKFLPLTNIEETLNNL 201	
QY	202	VNKIDVYLINAKKINDCNVEKDEBAHVKITLSLKAIDKIDLPKNYPDEAIKQLIND 261	
DB	357	VNKIDVYLINAKKINDCNVEKDEBAHVKITLSLKAIDKIDLPKNYPDEAIKQLIND 261	
QY	262	DTKQMLGKLLSTGLVONFPNTIISKLEGFQDMNLSOHQCVKQCPENSGCFRHLDE 416	
DB	417	DTKQMLGKLLSTGLVONFPNTIISKLEGFQDMNLSOHQCVKQCPENSGCFRHLDE 416	
QY	322	RESECKLANKQSGDKCVENPNPTCNENNGCCADATCTEEDSSSKRTTCECTKDSY 381	
DB	477	RESECKLANKQSGDKCVENPNPTCNENNGCCADATCTEEDSSSKRTTCECTKDSY 381	
QY	382	PLFDGIFGCS 391	
DB	537	PLFDGIFGCS 546	

RESULT 5  
 US-09-710-000-8  
 Sequence 8, Application US/09710000  
 Patent No. 6860498  
 GENERAL INFORMATION:  
 APPLICANT: Hul, George, S.N.  
 APPLICANT: Ho, Walter K.K.  
 APPLICANT: Lap-Yin, Pang  
 TITLE OF INVENTION: Malaria Vaccine  
 FILE REFERENCE: 23461-2001100  
 CURRENT APPLICATION NUMBER: US/09/710,000  
 PRIOR FILING DATE: 2000-11-10  
 PRIOR APPLICATION NUMBER: 60/226,861  
 PRIOR FILING DATE: 2000-08-22  
 PRIOR APPLICATION NUMBER: 60/165,178  
 PRIOR FILING DATE: 1999-11-12  
 PRIOR APPLICATION NUMBER: 60/168,327  
 PRIOR FILING DATE: 1999-12-11  
 NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 8  
 LENGTH: 375  
 TYPE: PRT  
 ORGANISM: Unknown  
 FEATURE:  
 OTHER INFORMATION: amino acid sequence of PfMSP-142  
 US-09-710-000-8

Query Match  
 Best Local Similarity 95.1%; Score 1970; DB 2; Length 375;  
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	17	MAISVTMDNITSGFENEYDVYIKPLAGYRSLSKQIEKNITFTFNINDILNSRLKRRK 76
DB	1	MAISVTMDNITSGFENEYDVYIKPLAGYRSLSKQIEKNITFTFNINDILNSRLKRRK 76
QY	77	YFLDVLSDMLMOFGHISSENYIIEISFRLNSSEKNTLSKYKIKESVENDIKFAOGI 136
DB	61	YFLDVLSDMLMOFGHISSENYIIEISFRLNSSEKNTLSKYKIKESVENDIKFAOGI 120
QY	137	SYEKVLAKYKXDLSEIKYIKERKEKFPSSPTTPSPAKTDEOKKESKFLPLTNIEET 196
DB	121	SYEKVLAKYKXDLSEIKYIKERKEKFPSSPTTPSPAKTDEOKKESKFLPLTNIEET 180
QY	197	VNKLINAKKINDCNVEKDEBAHVKITLSLKAIDKIDLPKNYPDEAIKQLIND 240
DB	181	VNKLINAKKINDCNVEKDEBAHVKITLSLKAIDKIDLPKNYPDEAIKQLIND 240
QY	257	KLINDTKQMLGKLLSTGLVONFPNTIISKLEGFQDMNLSOHQCVKQCPENSGCF 316
DB	241	KLINDTKQMLGKLLSTGLVONFPNTIISKLEGFQDMNLSOHQCVKQCPENSGCF 300
QY	317	RHLDERECKLANKQSGDKCVENPNPTCNENNGCCADATCTEEDSSSKRTTCECT 376
DB	301	RHLDERECKLANKQSGDKCVENPNPTCNENNGCCADATCTEEDSSSKRTTCECT 360
QY	377	KPDGIFGCS 391
DB	361	KPDGIFGCS 391

RESULT 6  
 US-10-057-531A-5  
 Sequence 5, Application US/10057531A  
 Patent No. 6855322  
 GENERAL INFORMATION:  
 APPLICANT: Lyon, Jeffrey A.  
 APPLICANT: Angov, Evelina  
 TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite  
 FILE REFERENCE: 003/241/SAP  
 CURRENT APPLICATION NUMBER: US/10/057,531A  
 PRIOR FILING DATE: 2002-01-25  
 PRIOR APPLICATION NUMBER: US 60/264,535  
 PRIOR FILING DATE: 2001-01-26  
 PRIOR APPLICATION NUMBER: US 60/347,564  
 PRIOR FILING DATE: 2001-10-26  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: Apple Macintosh Microsoft Word 6.0  
 SEQ ID NO 5  
 LENGTH: 383  
 TYPE: PRT  
 ORGANISM: Plasmodium falciparum 3D7 MSP142  
 US-10-057-531A-5

Query Match  
 Best Local Similarity 99.2%; Score 1968; DB 2; Length 383;  
 Matches 376; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	13	SGGTMAISVTMDNITSGFENEYDVYIKPLAGYRSLSKQIEKNITFTFNINDILNSRL 72
DB	5	SGGTMAISVTMDNITSGFENEYDVYIKPLAGYRSLSKQIEKNITFTFNINDILNSRL 64

**THIS PAGE BLANK (USE)**